

DIAGNOSIS OF METASTATIC CANCER BY THE MTS-1 GENE

CROSS-REFERENCE TO RELATED APPLICATIONS

5                   This is a Continuation-In-Part of U.S.S.N.  
08/468,942 filed June 6, 1995, which is a Divisional of  
U.S.S.N. 190,560 filed January 31, 1994, which is a  
Continuation-In-Part of U.S.S.N. 981,455 filed November  
25, 1992, which is a Rule 60 Continuation of U.S.S.N.  
10                  550,600 filed July 9, 1990.

FIELD OF THE INVENTION

15                   The present invention is directed towards the  
diagnosis of malignant cancer by detection of the mts-1  
mRNA or the mts-1 protein encoded by the mts-1 gene.  
This invention further relates to cancer therapeutics.  
More particularly, this invention relates to compositions  
and methods for treating tumors, for example, by  
20                  intercepting the interaction between Mts-1 and p53. The  
present invention is also directed to mammalian cell  
lines and tumors with high and low metastatic potential  
which have been developed to serve as useful model  
systems for in vitro and in vivo anti-metastasis drug  
25                  screening.

BACKGROUND OF THE INVENTION

30                   Malignant cancer tumors shed cells which  
migrate to new tissues and create secondary tumors; a  
benign tumor does not generate secondary tumors. The  
process of generating secondary tumors is called  
metastasis and is a complex process in which tumor cells

colonize sites distant from the primary tumor. Tumor  
metastasis remains the major cause of morbidity and death  
for patients with cancer. One of the greatest challenges  
in cancer research is to understand the basis of  
5 metastasis, i.e., what controls the spread of tumor cells  
through the blood and lymphatic systems and what  
allows tumor cells to populate and flourish in new  
locations.

The metastatic process appears to be sequential  
10 and selective, and is controlled by a series of steps  
since metastatic tumor cells: (a) are mobile and can  
disseminate from the original tumor; (b) are capable of  
invading the cellular matrix and penetrating through  
blood vessels; (c) possess immunological markers, which  
15 allow them to survive passage through the blood stream,  
where they must avoid the immunologically active  
cytotoxic "T" lymphocytes; and (d) have the ability to  
find a favorable location to transplant themselves and  
successfully survive and grow.

20 Understanding the underlying molecular  
mechanisms in metastasis is the key to understanding  
cancer biology and its therapy. In clinical lesions,  
malignant tumors contain a heterogeneous population of  
cells, exhibiting a variety of biological  
25 characteristics, e.g., differential growth rates, cell  
surface structures, invasive capacities and sensitivity  
to various cytotoxic drugs. Researchers can take  
advantage of tumor heterogeneity factors, by identifying  
specific cell produced markers, which are unique for  
30 metastasis, to develop therapeutic regiments which do not  
rely only on surgical resection.

At this time it is not known whether the metastatic phenotype is under the regulation of a single or multiple gene(s), and whether these genes are independent or interrelated. However, a number of genes have become correlated with the formation and metastasis of tumors. For example, several normal cellular genes become oncogenes by incorporation into a retroviral genome. Due to the juxtaposition of new promoter elements, such incorporation frequently allows a potential oncogene to be expressed in inappropriate tissues or at higher levels than it normally would be expressed. It appears from work with tumorigenic retroviruses as well as other systems that misexpression of many cellular proteins, particularly those involved in the regulation of the cell cycle, cell mobility, or cell-cell interaction may lead to a cancerous phenotype.

The present invention discloses the human mts-1 gene and diagnosis of metastatic cancer by use of either antibodies directed against the mts-1 protein or mts-1 nucleic acid probes directed against mts-1 mRNA.

The mouse and rat mts-1 genes have been previously isolated under different names (i.e., 18A2, Linzer, et al., Proc. Natl. Acad. Sci. USA. 80:4271-4275, 1983; and p9Ka, Barraclough et al., J. Mol. Biol. 198:13-20, 1987) but no function or correlation of the mts-1 gene in metastatic cancer has been established prior to the present invention. Previous work has indicated that the protein now identified as the mts-1 protein is a calcium binding protein with homology to other calcium binding proteins such as, for example, the S-100 calcium protein, which are thought to have a role in cell growth (Linzer et al. supra; Jackson-Grusby et

al., Nuc. Acids Res. 15:6677-6690, 1987; Goto et al., J. Biochem. 103:48-53, 1988). Other researchers suggest a role for p9Ka, later found to be identical to mts-1, in myoepithelial cell differentiation (Barracclough, et al., supra).

As determined uniquely by the present invention, the mammalian mts-1 gene is expressed at 10-100 fold higher levels in metastatic cells compared to non-metastatic cells and normal cells. Only a few types of normal cells, including lymphocytes and trophoblasts, express mts-1. Hence, the present invention demonstrates a surprising new property of mts-1: the misexpression of mts-1 within a cell or tissue is diagnostic of malignant cancer.

p53 is a tumor suppressor protein found in humans and other mammals (See, e.g., Harris, *Science* 262: 1980-1981, 1993). The wild-type p53 protein functions to regulate cell proliferation and cell death (also known as apoptosis). While the mechanism through which the wild-type p53 protein suppresses tumor cell growth is not completely defined, it is known that one key feature of the growth suppression is the capacity of p53 to act as a transcription factor (Farmer et al., *Nature* 358, 83-86, 1992; and Kern et al., *Science* 256, 827-830, 1992).

The nucleotide and amino acid sequences of human p53 have been reported by Zakut-Houri et al, *EMBO J.* 4: 1251-1255, 1985). The ability of p53 to bind DNA in a sequence-specific manner maps to amino acid residues 90-290 of human p53 (Pavletich et al, *Genes Dev.* 7: 2556-2564, 1993; and Wang et al, *Genes Dev.* 7: 2575-2586



1993); the tetramerization domain maps to amino acid  
residues 322-355 of human p53. The DNA binding-  
regulation domain maps to amino acid residues 364-393 of  
human p53 or to the corresponding region encompassing  
residues 361-390 of mouse p53 (Hupp et al., *Cell* 71: 875-  
886, 1992; and Halazonetis et al., *EMBO J.* 12: 1021-1028,  
1993).

Inactivation of p53 is associated with more  
than half of all human tumors. The inactivation can  
occur by mutation of the p53 gene or through binding of  
p53 to viral or cellular oncogene proteins, such as the  
SV40 large T antigen and MDM2. Mutations of the p53  
protein in most human tumors involve the sequence-  
specific DNA binding domain (Bargonetti et al., *Genes*  
*Dev.* 6: 1886-1898, 1992).

The present invention has further identified  
the tumor suppressor protein p53 as a target for the  
metastasis associated Mts1 protein.

#### SUMMARY OF THE INVENTION

The present invention is directed towards the  
diagnosis of metastatic cancer using an mts-1 nucleic  
acid or antibodies directed against the mts-1 protein.  
The present invention is also directed to isolated and  
purified mts-1 nucleic acids available for diagnostic  
tests and antibodies directed against the mammalian mts-1  
proteins.

One aspect of the present invention is directed  
to a method for diagnosing metastatic cancer by  
contacting serum from an individual to be tested for such

cancer with an antibody reactive with a mammalian mts-1 protein or an antigenic fragment thereof, for a time and under conditions sufficient to form an antigen-antibody complex, and detecting the antigen-antibody complex.

5           Another aspect of the present invention provides an isolated, recombinant nucleic acid encoding a human mts-1 gene or a fragment thereof, and replicable DNA sequences encoding an mts-1 polypeptide which express high levels of the mts-1 polypeptide. Isolated antisense  
10 mts-1 nucleic acids and expression vectors therefor are also contemplated by the present invention. Human mts-1 nucleic acids are preferred.

15           A further aspect of this invention is directed to isolated transformed host cells, such as prokaryotic microorganisms, yeast, insect cells and eukaryotic cells, containing mts-1 nucleic acids and replicable vectors containing DNA sequences encoding the mts-1 polypeptide.

20           A still further aspect of this invention provides isolated homogeneous mammalian mts-1 polypeptides and pharmaceutical compositions including such a mts-1 polypeptide or protein. Human mts-1 polypeptides are preferred.

25           Another aspect of this invention provides antibodies directed against an mts-1 polypeptide or any peptide, fragment or derivative of the mts-1 protein.

30           A further aspect of this invention is directed towards treatment of cancer by administering reagents, such as for example, anti-mts-1 antibodies capable of binding the mts-1 protein and antisense mts-1 nucleic acids capable of binding mts-1 sense mRNA.

One aspect of the invention provides compounds which interfere with the interaction between Mts-1 and p53 by binding to Mts-1 (i.e., binding-intercepting compounds).

5 Another embodiment of the present invention provides a method for intercepting the binding between p53 and Mts-1 in a subject by administering to the subject, an effective amount of a peptide which prevents the interaction between p53 and Mts-1 by binding to Mts-1. For example, one such peptide comprises the C-terminal region of p53 (amino acid 289-393 of human p53 or amino acid 289-390 of murine p53), in particular, amino acid 360-393 of human p53 or amino acid 360-390 of murine p53. Functional fragments or analogs of such peptides are also within the scope of the present invention. Another example of a binding-intercepting peptide comprises amino acid 1909-1937 of non-muscle myosin heavy chain or functional fragments of analogs thereof.

20 In one embodiment, the present invention provides methods of treating a tumor in a subject by administering to the subject, a therapeutically effective amount of a nucleic acid molecule coding for a peptide which prevents the binding of Mts-1 to p53.

25 In one embodiment, the present invention provides methods of treating a tumor in a subject by administering to the subject, a therapeutically effective amount of a peptide which prevents the binding of Mts-1 to p53.

In another embodiment, the present invention provides a method of treating a tumor in a subject by administering to the subject, a therapeutically effective amount of an antibody directed against Mts-1.

5 In still another embodiment, the present invention provides methods of treating a tumor in a subject by administering a therapeutically effective amount of an antisense DNA of an Mts-1 gene.

10 Yet another aspect of the present invention provides an animal model system of the metastatic process, including several eukaryotic cell lines and tumors expressing different levels of mts-1, which are derived from mouse and rat carcinomas. These cell lines and tumors may be re-introduced into mice or rats to  
15 produce primary tumors which metastasize to the lung, liver and kidneys with a characteristic frequency. Therefore, the present invention also provides a well controlled animal model system for testing pharmaceutical compositions suspected to have therapeutic utility for  
20 the treatment of metastatic cancer.

#### BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 depicts the nucleotide sequence of the coding region of the human mts-1 gene.

25 FIG. 2 depicts the amino acid sequence of the human mts-1 protein.

FIG. 3 depicts the circular, expression plasmid pEMSVscribe2 containing the complete coding region of mts-1 under the control of the murine sarcoma virus promoter (MSV LTR).  
30

FIG. 4 illustrates an autoradiograph showing detection of the mts-1 transcript by a mts-1 nucleic acid probe in a Northern blot of mRNA from a cell line with low metastatic potential (CSML-0) and a cell line with very high metastatic potential (CSML-100).

FIG. 5 illustrates an autoradiograph showing detection of the mts-1 transcript by a mts-1 nucleic acid probe in a Northern blot of mRNA from different metastatic (depicted with an "M" above the lane) and non-metastatic mouse tumors and cell lines. In the top autoradiograph: Lane 1-HMC-Lr; Lane 2-HMC-0; Lane 3-RL-67; Lane 4-B-16, Lane 5-LLC; Lane 6-Acatol; Lane 7-C12; Lane 8-PCC4c-B; Lane 9-PCC4c-P, Lane 10-PCC4c-107; Lane 11-PCC4107; Lane 12-T9; Lane 13-LMEC; Lane 14-T36; Lane 15-T36cL. The bottom autoradiograph depicts the same Northern blot hybridized with an actin probe, providing a comparison of the amounts of mRNA in each lane.

FIG. 6 illustrates an autoradiograph showing detection of the mts-1 transcript by a mts-1 nucleic acid probe in a Northern blot of mRNA from various tumors and tumor cell lines. Lanes 1 and 2-size markers; Lane 3-mouse lung carcinoma Line 1 grown without DMSO; Lane 4-mouse lung carcinoma Line 1 grown with 3% DMSO; Lane 5-IR6 tumor; Lane 6-TRCL<sub>1</sub> cell line; Lane 7-IR6 cell line (IR6CL<sub>1</sub>); Lane 8-FRTL5 cell line.

FIG. 7 depicts a histopathological characterization of some of the rat tumors of the present invention, demonstrating the morphological and histological identity of these tumors with corresponding human tumors.

FIG. 8 illustrates an autoradiograph showing detection of the mts-1 transcript by a mts-1 nucleic acid

probe in a Northern blot of mRNA from various Line 1 murine lung carcinoma cell lines containing a transfected copy of the rat mts-1 gene (N1-N10), or just an antibiotic resistance marker (Neo 1-3), all grown in the present of 3% DMSO; compared to Line 1 cells grown without DMSO (Line 1). DMSO inhibits the development of the metastatic phenotype as well as mts-1 expression in non-transfected Line 1 cells, hence transfection of mts-1 can overcome this block.

FIG. 9a depicts the lungs from 3 mice injected subcutaneously with  $1 \times 10^6$  CSML-0 cells. Lungs were removed 4-6 weeks after injection and then injected with India ink. Dark areas indicate normal tissues; white areas are tumors.

FIG. 9b depicts the lungs from 3 mice injected intravenously with  $1 \times 10^4$  CSML-0 cells. Lungs were removed 15 days after injection and then injected with India ink. Dark areas indicate normal tissues; white areas are tumors.

FIG. 9c depicts the lungs from 3 mice injected intravenously with  $1 \times 10^4$  CSML-100 cells. Lungs were removed 15 days after injection and then injected with India ink. Dark areas indicate normal tissues; white areas are tumors.

FIG. 9d depicts the lungs from 3 mice injected subcutaneously with  $1 \times 10^6$  CSML-100 cells. Lungs were removed 4-6 weeks after injection and then injected with India ink. Dark areas indicate normal tissues; white areas are tumors.

FIG. 9e depicts the lungs from 3 mice injected with 0.1 ml serum-free media. Lungs were removed 6-8 weeks after injection and then injected with India ink.

Dark areas indicate normal tissues; white areas are tumors.

FIG. 10a depicts a diagram of the more important regions of the pTrcHis B expression vector utilized to produce a histidine-*mts-1* fusion protein. The murine *mts-1* cDNA was subcloned into pTrcHis B at the BamHI-KpnI site to generate pTBM1.

FIG. 10b depicts a Coomassie Brilliant Blue-stained gel illustrating the profile of proteins eluted from a Ni<sup>++</sup>-NTA column used to purify *mts-1* protein expressed by cells containing pTBM1. Elution was with a series of buffers having pH values varying from 5.9 to 4.5. A single major protein, the *mts-1* protein, is eluted.

FIG. 11 depicts a growth curve of CSML-0 and CSML-100 cells over a five day period. Cell growth was measured daily by observing the number of cells per dish (ordinate). As illustrated, CSML-100 cells, which express high levels of *mts-1*, grow at a slower rate than CSML-0 cells which express little *mts-1*.

FIG. 12a depicts a photomicrograph of a section from an 8 day mouse embryo hybridized with a <sup>3</sup>H-labelled *mts-1* antisense probe. Signal is detected in the trophoblast cells.

FIG. 12b depicts a photomicrograph of a section from an 8 day mouse embryo hybridized with a <sup>3</sup>H-labelled *mts-1* sense probe. No signal is detected.

FIG. 13 depicts a western blot of CSML-0 (Lane 1) and CSML-100 (Lanes 2 and 3) cell lysates. Lanes 1 and 2 were probed with the chicken anti-*mts-1* antibody ( $\alpha$ -*mts-1*) using a secondary antibody (rabbit anti-chicken IgG-HRP) for detection. Lane 3 was similarly probed

except that free mts-1 protein was added during the incubation with the  $\alpha$ -mts-1 antibody. An approximate 10-12 kd mts-1 protein is detected only in CSML-100 cells and only when no free mts-1 protein is present to compete for binding to the  $\alpha$ -mts-1 antibody. Therefore, the  $\alpha$ -mts-1 antibody is highly specific for mts-1 protein.

FIG. 14a depicts a frozen mouse spleen section probed with the  $\alpha$ -mts-1 antibody. Rabbit anti-chicken IgG-HRP was used for detection of the mts-1 antigen-antigen complex (dark spots).

FIG. 14b depicts a frozen mouse spleen section probed with the  $\alpha$ -mts-1 antibody in the presence of free mts-1 protein. Rabbit anti-chicken IgG-HRP was used for detection of the mts-1 antigen-antigen complex (dark spots). As illustrated, little or no mts-1 protein is detected when free mts-1 protein is present to compete for binding to  $\alpha$ -mts-1 (compare to FIG. 14a). Therefore, the  $\alpha$ -mts-1 antibody is highly specific for mts-1 protein.

FIG. 15a illustrates that mts-1 protein can be detected only in serum from mice injected with CSML-100 cells. This figure depicts a western blot of serum taken from non-injected mice (Lane 3), mice injected with  $1 \times 10^5$  CSML-0 cells (Lane 1) and mice injected with  $1 \times 10^5$  CSML-100 cells (Lane 2). After reaction with the  $\alpha$ -mts-1 antibody a 10-12 kd mts-1 protein is detected only in the serum from mice injected with CSML-100 cells. The higher molecular weight bands merely cross-react with the anti-mts-1 antibody used and were not mts-1 proteins.

FIG. 15b similarly illustrates that mts-1 protein can be detected only in serum from mice injected with CSML-100 cells. This figure depicts a western blot



of serum taken from non-injected mice (Lane 3), mice injected with  $1 \times 10^6$  CSML-0 cells (Lane 1) and mice injected with  $1 \times 10^6$  CSML-100 cells (Lane 2). After reaction with the  $\alpha$ -mts-1 antibody a 10-12 kd mts-1 protein is detected only in the serum from mice injected with CSML-100 cells. As described, the higher molecular weight bands merely cross-react with the anti-mts-1 antibody used and were not mts-1.

FIG. 15c depicts a western blot of lysed whole blood from mice probed with the  $\alpha$ -mts-1 antibody. Lanes 1-4 were loaded with 5, 10, 20 and 25  $\mu$ l lysed whole blood, respectively. Lane 5 was loaded with CSML-100 cell lysate as a positive control. This blot illustrates that mts-1 protein in serum is not simply due to lysis of lymphocyte or blood cells.

FIG. 15d depicts a western blot of increasing amounts of serum from mice injected with salmonella lipopolysaccharide (LPS) to induce a chronic immune response. The blot was probed with the  $\alpha$ -mts-1 antibody to reveal any detectable mts-1 protein. Lanes 1-3 were loaded with 75, 100 or 150 $\mu$ g serum, respectively. This blot illustrates that mts-1 protein in serum is not derived from activated macrophages generated by a chronic immune response.

FIG. 16 depicts a western blot of sera from patients with non-metastatic and metastatic cancers probed with the  $\alpha$ -mts-1 antibody to reveal any detectable mts-1 protein. A 27 kd mts-1 protein is detected only in patients known to have metastatic cancer. Sera were taken from patients with non-metastatic breast cancer (Lane 1), with non-metastatic lymphomas (Lanes 2 and 4), with metastatic lymphomas (Lanes 5 and 7) and with metastatic

breast cancer (Lane 6). Lane 3 contains normal serum as a negative control. The higher molecular weight proteins merely cross-react with the  $\alpha$ -mts-1 antibody and do not represent mts-1 protein products.

5           FIG. 17 depicts co-immunoprecipitation of Mts1 and p53.

10           Top panel- CSML-100 lysates immunoprecipitated by different batches of anti-Mts1 antibody (1-4) and control antibody (C). Antibodies 3 and 4 effectively pulled down Mts1-protein complexes with Myosin (200kDa) and p53 (53kDa). Antibodies 1 and 4 are less effective for complex IP.

15           Bottom panel- Cells were metabolically labelled with  $^{35}$ S-Methionin and immunoprecipitation was performed using: lysate from CSML-100 cells + anti-Mts1 serum (lane 1); lysate from CSML-100 cells + control antibody (lane 2); lysate from CSML-0 cells + pAb 421 (lane 3); lysate from CSML-100 cells + pAb 421 (lane 4).

20           FIG. 18 depicts immunoprecipitation of non-labeled Mts-1 from CSML-100 cells using anti-p53 antibodies directed to various epitopes.

25           FIG. 19 depicts the interaction between Mts1 and the C-terminal domain of p53. Full size recombinant p53 and its domains were mixed with recombinant Mts1 and pooled-down with anti-p53 antibodies. Western blot was performed with immunoprecipitates followed by immunoprob-  
30           ing with anti-Mts1 antibody. Lanes 1,2 -full size p53; 3,4 -N-terminal domain; 5,6 -DNA-binding domain; 7,8 -C-terminal domain; and in 1,3,5 and 7 - control antibody was used.

FIG. 20 depicts binding of the recombinant Mts1 to p53-GST fusion proteins fixed on Glutathione-sepharose beads. Mts1 associated with GST (negative control), GST-p53 (wild type p53) and GST-p53-Δ30 (mutated p53 lacking amino acids 364-393) was analyzed by Western blot with following immunoprobings with anti-mts1 antibody.

FIG. 21 depicts Mts1 interaction with target proteins in a blot-overlay assay. Recombinant full size p53 (1), N-terminal domain (2), DNA-binding domain (3), C-terminal domain (4) and the fragment of the non-muscle myosin (5) after gel electrophoresis were transferred onto nitrocellulose membrane. Identical membranes were incubated with different batches of the recombinant Mts1 protein (Mts1-a, Mts1-b, Mts1-c and Mts1-d). Mts1 bound to the fixed proteins was detected by the anti-Mts1 serum. The graph at the upper left depicts the schematic localization of the proteins on the membranes.

FIG. 22 depicts the Mts-1 inhibition of p53 phosphorylation by PKC on the C-terminal domain in vitro.

Top - phosphorylation of full size recombinant p53 in the presence and absence of recombinant Mts1.

Bottom - phosphorylation of the N-terminal domain (left), the DNA-binding domain (middle) and the C-terminal domain of P53 in presence of Mts1 (with increasing Mts concentrations from left lanes to right lanes in each radiography).

FIG. 23 depicts phosphorylation by CKII full size p53 (lanes 1,2) and C-terminal domain of p53 (lanes 3,4) in the absence (lanes 1,3) and presence (lanes 2,4).

of the recombinant Mts1. Left panel: autoradiography of the dried gel; right panel - Coomassie staining of the same gel.

FIG. 24 depicts EMSA using CSML-0 nuclear extracts with p53 binding site from p21/WAF1 promoter.

FIG. 25A depicts the inhibition by Mts1 of the p53 transactivation of the p21/WAF2-luciferase reporter gene in CSML-0 cells. CSML-0 cells were transiently transfected with p21-luc along with p53 and mts1. Cells were collected in 24 hours and relative luciferase activity was determined.

FIG. 25B depicts transactivation of p53-responsive reporters in Sao-2 cells. Cells were transiently transfected with p21-luc along with p53 and/or mts1. Cells were collected in 24 hours and relative luciferase activity was determined.

FIG. 26 depicts the effects of anti-Mts1 antibody administered to mice bearing highly metastatic CSML-100 tumors.

#### DETAILED DESCRIPTION OF THE INVENTION

The present invention provides a new method for diagnosing metastatic cancer and for distinguishing metastatic tumors from benign tumors. In particular, the present invention demonstrates a heretofore unknown property of a mammalian gene, called mts-1, whose expression is about 10 to about 100 fold higher in metastatic tumor cells, for example, of the lung, liver, kidney, mammary gland, epithelial, thyroid, leukemic, pancreatic, endometrial, ovarian, cervical, skin, colon

or lymphoid tissue than in benign tumor cells or the  
corresponding normal cells. According to the present  
invention metastatic cancer of these and other tissues  
can be detected in patient's serum by a simple  
5 immunoassay. Moreover, metastatic cancer can also be  
diagnosed in tissue biopsies by the present immunoassays  
or by in situ hybridization assays.

Metastasis is the formation of secondary tumors  
by cells derived from a primary tumor. The metastatic  
10 process involves mobilization and migration of primary  
tumor cells from the site of the primary tumor into new  
tissues where the primary tumor cells induce the  
formation of secondary (metastatic) tumors. In accordance  
with the present inventive discovery, the increased  
15 expression of the mts-1 gene in a cell or tissue is  
strongly indicative of metastatic potential. The present  
invention utilizes this unexpected and surprising  
correlation of high mammalian mts-1 gene expression with  
high metastatic potential to detect or diagnose malignant  
20 cancer. Both the mammalian mts-1 nucleic acid and  
antibodies directed against mammalian mts-1 proteins are  
contemplated for use in the diagnosis of malignant  
cancer. The human mts-1 gene, depicted by one of the  
nucleotide sequences below, has been isolated for the  
25 first time in the present invention.

SEQ ID NO:1

ATG-GCG-TGC-CCT-CTG-GAG-AAG-GCC-CTG-GAT'GTG-ATG-GTG-TCC-  
ACC-TTC-CAC-AAG-TAC-TCG-GGC-AAA-GAG-GGT-GAC-AAG-TTC-AAG-  
30 CTC-AAC-AAG-TCA-GAG-CTA-AAG-GAG-CTG-CTG-ACC-CGG-GAG-CTG-  
CCC-AGC-TTC-TTG-GGG-AAA-AGG-ACA-GAT-GAA-GCT-GCT-TTC-CAG-  
AAG-CTG-ATG-AGC-AAC-TTG-GAC-AGC-AAC-AGG-GAC-AAC-GAG-GTG-

GAC-TTC-CAA-GAG-TAC-TGT-GTC-TTC-CTG-TCC-TGC-ATC-GCC-ATG-  
 ATG-TGT-AAC-GAA-TTC-TTT-GAA-GGC-TTC-CCA-GAT-AAG-CAG-CCC-  
 AGG-AAG-AAA; or

5 SEQ ID NO:3

GGC-AGT-TGA-GGC-AGG-AGA-CAT-CAA-GAG-AGT-ATT-TGT-GCC-  
 CTC-CTC-GGG-TTT-TAC-CTT-CCA-GCC-GAG-ATT-CTT-CCC-CTC-  
 TCT-ACA-ACC-CTC-TCT-CCT-CAG-CGC-TTC-TTC-TTT-CTT-GGT-  
 10 TTG-ATC-CTG-ACT-GCT-GTC-ATG-GCG-TGC-CCT-CTG-GAG-AAG-  
 GCC-CTG-GAT-GTG-ATG-GTG-TCC-ACC-TTC-CAC-AAG-TAC-TCG-  
 GGC-AAA-GAG-GGT-GAC-AAG-TTC-AAG-CTC-AAC-AAG-TCA-GAA-  
 CTA-AAG-GAG-CTG-CTG-ACC-CGG-GAG-CTG-CCC-AGC-TTC-TTG-  
 GGG-AAA-AGG-ACA-GAT-GAA-GCT-GCT-TTC-CAG-AAG-CTG-ATG-  
 15 AGC-AAC-TTG-GAC-AGC-AAC-AGG-GAC-AAC-GAG-GTG-GAC-TTC-  
 CAA-GAG-TAC-TGT-GTC-TTC-CTG-TCC-TGC-ATC-GCC-ATG-ATG-  
 TGT-AAC-GAA-TTC-TTT-GAA-GGC-TTC-CCA-GAT-AAG-CAG-CCC-  
 AGG-AAG-AAA-TGA-AAA-CTC-CTC-TGA-TGT-GGT-TGG-GGG-GTC-  
 TGC-CAG-CTG-GGG-CCC-TCC-CTG-TCG-CCA-GTG-GGC-ACT-TTT-  
 20 TTT-TTT-CCA-CCC-TGG-CTC-CTT-CAG-ACA-CGT-GCT-TGA-TGC-  
 TGA-GCA-AGT-TCA-ATA-AAG-ATT-CTT-GGA-AGT-TTA,  
 wherein SEQ ID NO:3 is different from SEQ ID NO:1 at the  
 underlined positions.

25 The amino acid sequence of the human mts-1  
 protein is depicted below (SEQ ID NO:2):

Met-Ala-Cys-Pro-Leu-Glu-Lys-Ala-Leu-Asp-Val-Met-Val-Ser-  
 Thr-Phe-His-Lys-Tyr-Ser-Gly-Lys-Glu-Gly-Asp-Lys-Phe-Lys-  
 Leu-Asn-Lys-Ser-Glu-Leu-Lys-Glu-Leu-Leu-Thr-Arg-Glu-Leu-  
 30 Pro-Ser-Phe-Leu-Gly-Lys-Arg-Thr-Asp-Glu-Ala-Ala-Phe-Gln-  
 Lys-Leu-Met-Ser-Asn-Leu-Asp-Ser-Asn-Arg-Asp-Asn-Glu-Val-  
 Asp-Phe-Gln-Glu-Tyr-Cys-Val-Phe-Leu-Ser-Cys-Ile-Ala-Met-

Met-Cys-Asn-Glu-Phe-Phe-Glu-Gly-Phe-Pro-Asp-Lys-Gln-Pro-Arg-Lys-Lys.

5 Other mammalian mts-1 genes are also contemplated.

10 The present invention also relates to a useful animal model system of metastasis for screening potential antimetastatic drugs and for developing therapeutic regimens for cancer treatment. This model system includes non-metastasizing and metastasizing tumors that are maintained by sequential transplantation from one mouse or rat to another, as well as cultured cell lines, derived from these tumors, which retain the metastatic or non-metastatic potential of their parental tumors. Hence, 15 these tumors or cell lines may be transplanted or injected into mice or rats to generate benign or metastatic tumors. Concurrently, drugs or other therapies with anti-tumorigenic or anti-metastatic potential, may be introduced into the animal to test whether the 20 formation of the metastatic and benign tumors is suppressed. This model system has high utility because of the predictable metastatic potential of the tumors and cell lines therein and also because cell lines of differing metastatic potential were derived from the same 25 parental tumor and hence have a common genetic and phenotypic make-up, except for their metastatic potential. Hence the animal model system of the current invention is highly controlled and has predictable metastatic potential.

30 The human mts-1 gene of the present invention was obtained by use of mouse and rat mts-1 clones previously obtained by the present inventors. The mouse

and rat mts-1 genes were obtained from cDNA libraries made from metastatic mouse and rat tumor RNAs. The mouse mts-1 gene has been obtained from a highly metastatic cell line derived from a spontaneous mouse mammary carcinoma (CSML-100), while the mts-1 rat gene utilized in the present invention was from a highly metastatic thyroid carcinoma, IR-6. Both the mouse and rat mts-1 genes were obtained by differential hybridization of the respective cDNA libraries with a probe made from a pool of mRNAs from highly metastatic tissues, and a probe made from a pool of mRNAs from low metastatic tissues.

The human mts-1 gene was obtained from a cDNA library made by the present inventors from mRNA purified from cultured HeLa cells and from cultured melanoma Wm64 cells. Clones hybridizing strongly to a mouse mts-1 cDNA probe can be identified as being the human mts-1 homologue by DNA sequencing. Alternatively, a cDNA can be obtained by reverse transcription and polymerase chain reaction using mRNA purified from metastatic cells, e.g. as provided in Miller 1988 Ann. Rev. Microbiol. 42: 177.

There is a difference of seven amino acids between the mouse and human mts-1 proteins, demonstrating that while the mouse and human proteins are functionally related they are not identical structurally.

In another embodiment, the mouse, rat, and, in particular, the human mts-1 genes of the present invention have been subcloned into convenient replicable vectors for production of large amounts of mts-1 DNA and large amounts of sense or antisense mts-1 RNA. Convenient replicable vectors comprise the gene or a DNA fragment thereof of the present invention, an origin of replication which is operable in the contemplated host,



and, preferably, a selectable marker, for example, an antibiotic resistance marker. Many of these vectors are based on pBR322. Convenient replicable vectors which allow synthesis of RNA from the DNA of interest include Bluescript.TM. (commercially available from Stratagene), pTrcHisB (Invitrogen) and others that are well known in the art.

The present invention also contemplates replicable expression vectors allowing a higher level of expression of the mammalian mts-1 protein. Replicable expression vectors as described herein are generally DNA molecules engineered for controlled expression of a desired gene, especially high level expression where it is desirable to produce large quantities of a particular gene product, or polypeptide. The vectors encode promoters and other sequences to control expression of that gene, the gene being expressed, and an origin of replication which is operable in the contemplated host. Preferably the vector also encodes a selectable marker, for example, antibiotic resistance. Replicable expression vectors can be plasmids, bacteriophages, cosmids and viruses. Any expression vector comprising RNA is also contemplated.

Preferred vectors of the present invention are derived from eukaryotic sources. Expression vectors that function in tissue culture cells are especially useful, but yeast vectors are also contemplated. These vectors include yeast plasmids and minichromosomes, retrovirus vectors, BPV (bovine papilloma virus) vectors, baculovirus vectors, SV40 based vectors and other viral vectors. SV40-based vectors and retrovirus vectors (e.g., murine leukemia viral vectors) are preferred.

Tissue culture cells that are used with eukaryotic replicable expression vectors include Sf21 cells, CV-1 cells, COS-1 cells, NIH3T3 cells, mouse L cells, HeLa cells and such other cultured cell lines known to one skilled in the art.

A baculovirus expression system can be used to produce large amounts of mts-1 polypeptides in cultured insect cells. The post-translational processing of polypeptides produced in such insect cells is similar to that of mammalian cells. Production of polypeptides in insects is therefore advantageous, particularly when one seeks to mimic the exact function or antigenic properties of the natural polypeptide. Moreover, mts-1 polypeptides expressed in the baculovirus system are produced without the need for a fused heterologous polypeptide because the mts-1 start codon is used as the translational start site.

Methods for producing polypeptides in the baculovirus expression system are known to the skilled artisan. See for example Miller 1988 Ann. Rev. Microbiol. 42: 177. In general, a modified Autographa californica nuclear polyhedrosis virus propagated in Sf21 cells is used for polypeptide expression. This modified virus is produced by cotransfection of a small transfer vector, encoding an mts-1 polypeptide, with a viral expression vector which has been linearized within an essential gene.

Once inside the cell, the linearized expression vector can undergo recombination with the transfer vector or simply recircularize. However, only recombination gives rise to viable viruses because the function of the essential gene is lost by recircularization. Recombinant

expression viruses are detected by formation of plaques. The present invention also contemplates prokaryotic vectors that may be suitable for expression of the mammalian mts-1 gene, including bacterial and bacteriophage vectors that can transform such hosts as E. coli, B. subtilis, Streptomyces sps. and other microorganisms. Many of these vectors are based on pBR322 including Bluescript.TM. (commercially available from Stratagene) and are well known in the art. Bacteriophage vectors that are used in the invention include lambda and M13.

Sequence elements capable of effecting expression of the human mts-1 gene include promoters, enhancer elements, transcription termination signals and polyadenylation sites. Promoters are DNA sequence elements for controlling gene expression, in particular, they specify transcription initiation sites. Prokaryotic promoters that are useful include the lac promoter, the trp promoter, and  $P_L$  and  $P_R$  promoters of lambda and the T7 polymerase promoter. Eukaryotic promoters are especially useful in the invention and include promoters of viral origin, such as the SV40 late promoter and the Moloney Leukemia Virus LTR, Murine Sarcoma Virus (MSV) LTR, yeast promoters and any promoters or variations of promoters designed to control gene expression, including genetically-engineered promoters. Control of gene expression includes the ability to regulate a gene both positively and negatively (i.e., turning gene expression on or off) to obtain the desired level of expression.

The replicable expression vectors of the present invention can be made by ligating part or all of

the mts-1 coding region in the sense or antisense orientation to the promoter and other sequence elements being used to control gene expression. This juxtapositioning of promoter and other sequence elements with the mts-1 gene allows the production of large amounts of sense or antisense mts-1 mRNA. Large amounts of the mts-1 protein can also be produced which are useful not only for anti-mts-1 antibody production but also for analysis of the function of mts-1 in metastatic cancer as well as for designing therapies for metastatic cancer.

As one example of an appropriate expression vector for the human mts-1 gene, the present invention provides the pEMSVscribe2 vector which expresses the human mts-1 gene of this invention.

In another example, large quantities of the mts-1 specific protein were expressed in an E. coli host using the inducible bacterial vector pTrcHisB (FIG. 10a). Murine mts-1 cDNA was subcloned in frame into a BamHI-KpnI site with the multiple cloning site of pTrcHisB to generate plasmid pTBM1. The fusion protein expressed by pTBM1 has 6 tandem histidine residues which allow easy purification of the fusion protein because of the high affinity of such tandem histidines for a Ni.sup.++ charged resin. The fusion protein also has an enterokinase specific cleavage site permitting removal of the histidines from the mts-1 protein product. Expression of the mts-1 fusion protein encoded by pTBM1 can be induced by IPTG. Similar human mts-1 cDNA constructs have also been generated.

Therefore, one skilled in the art has available many choices of replicable expression vectors, compatible

hosts and well-known methods for making and using the vectors. Recombinant DNA methods are found in any of the myriad of standard laboratory manuals on genetic engineering.

5           The present invention is also directed to the detection of metastatic cancer in tissue specimens by use of the mts-1 DNA as a nucleic acid probe for detection of mts-1 mRNA, or by use of antibodies directed against the mts-1 protein.

10           The nucleic acid probe of the present invention may be any portion or region of a mammalian mts-1 RNA or DNA sufficient to give a detectable signal when hybridized to mts-1 mRNA derived from a tissue sample. The nucleic acid probe produces a detectable signal  
15 because it is labeled in some way, for example because the probe was made by incorporation of nucleotides linked to a "reporter molecule".

          A "reporter molecule", as used in the present specification and claims, is a molecule which, by its  
20 chemical nature, provides an analytically identifiable signal allowing detection of the hybridized probe. Detection may be either quantitative or quantitative. The most commonly used reporter molecules in this type of  
25 assay are either enzymes, fluorophores or radionuclides covalently linked to nucleotides which are incorporated into a mts-1 DNA or RNA. Commonly used enzymes include horseradish peroxidase, alkaline phosphatase, glucose  
oxidase and  $\beta$ -galactosidase, among others. The substrates  
30 to be used with the specific enzymes are generally chosen for the production, upon hydrolysis by the corresponding enzyme, of a detectable color change. For example, p-nitrophenyl phosphate is suitable for use with alkaline

phosphatase conjugates; for horseradish peroxidase, 1,2-phenylenediamine, 5-aminosalicylic acid or toluidine are commonly used.

5 Incorporation into a mts-1 DNA probe may be by nick translation, random oligo priming, by 3' or 5' end labeling, by labeled single-stranded DNA probes using single-stranded bacteriophage vectors (e.g. M13 and related phage), or by other means, (Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual. Cold Spring Harbor Laboratory Press. Pages 10.1-10.70). Incorporation of a reporter molecule into a mts-1 RNA probe may be by synthesis of mts-1 RNA using T3, T7, Sp6 or other RNA polymerases (Sambrook et al., supra: 10.27-10.37).

15 Detection or diagnosis of metastatic cancer by the nucleic acid probe of the present invention can be by a variety of hybridization techniques which are well known in the art. In one embodiment, patient tissue specimens are sectioned and placed onto a standard microscope slide, then fixed with an appropriate fixative. The mts-1 RNA or DNA probe, labeled by one of the techniques described above, is added. The slide is then incubated at a suitable hybridization temperature (generally 37°C to 55°C) for 1-20 hours. Non-hybridized RNA or DNA probe is then removed by extensive, gentle washing. If a non-radioactive reporter molecule is employed in the probe, the suitable substrate is applied and the slide incubated at an appropriate temperature for a time appropriate to allow a detectable color signal to appear as the slide is visualized under light microscopy. 25 Alternatively, if the mts-1 probe is labeled radioactively, slides may be dipped in photoemulsion after hybridization and washing, and the signal detected 30

under light microscopy after several days, as exposed silver grains.

Metastatic cancer can also be detected from RNA derived from tissue specimens by the mts-1 nucleic acid probe. RNA from specimens can be fixed onto nitrocellulose or nylon filters, and well-known filter hybridization techniques may be employed for detection of mts-1 gene expression.

Specimen mRNA can be purified, or specimen cells may be simply lysed and cellular mRNA fixed unto a filter. Specimen mRNA can be size fractionated through a gel before fixation onto a filter, or simply dot blotted unto a filter.

In another embodiment, the mts-1 nucleic acid detection system of the present invention also relates to a kit for the detection of mts-1 mRNA. In general, a kit for detection of mts-1 mRNA contains at least one mts-1 nucleic acid. Such an mts-1 nucleic acid can be a probe having an attached reporter molecule or the mts-1 nucleic acid can be unlabelled. The unlabelled mts-1 nucleic acid can be modified by the kit user to include a reporter molecule or can act as a substrate for producing a labelled mts-1 probe, for example by nick translation or RNA transcription.

In another embodiment, the kit is compartmentalized: a first container can contain mts-1 RNA at a known concentration to act as a standard or positive control, a second container can contain mts-1 DNA suitable for synthesis of a detectable nucleic acid probe, and a third and a fourth container can contain reagents and enzymes suitable for preparing said mts-1 detectable probe. If the detectable nucleic acid probe is

made by incorporation of an enzyme reporter molecule, a fifth or sixth container can contain a substrate, or substrates, for the enzyme provided.

5 In accordance with the present invention, the mts-1 protein or portions thereof can be used to generate antibodies useful for the detection of the mts-1 protein in clinical specimens. Such antibodies may be monoclonal or polyclonal. Additionally, it is within the scope of this invention to include second antibodies (monoclonal or polyclonal) directed to the anti-mts-1 antibodies. The present invention further contemplates use of these antibodies in a detection assay (immunoassay) for the mts-1 gene product.

10 The present invention further contemplates antibodies directed against the mammalian, including rat, mouse and human, mts-1 proteins or polypeptides. These antibodies may be generated by using the entire mts-1 protein as an antigen or by using short peptides, encoding portions of the mts-1 protein, as antigens. When peptides are contemplated they have at least about 4 amino acids and preferably at least about 10 amino acids.

15 Preferably, specific peptides encoding unique portions of the mammalian mts-1 gene are synthesized for use as antigens for obtaining mts-1 antibodies. This is done because mts-1 encodes a calcium binding domain whose sequence, and hence antigenicity, is similar to other calcium binding proteins. By utilizing peptides encoding sequences lying outside the calcium binding domain, cross-reactivity of the anti-mts-1 antibodies towards other calcium binding proteins easily can be avoided. Accordingly, peptide sequences are tested for sequence homologies by searching protein sequence data banks



before peptides are actually synthesized. Among the various mts-1 peptides that can be used, four peptides encoding a portion of the human mts-1 sequence shown below, have already been used to generate antibodies:

5

- 1) Unique peptide encoding amino acids 2-11 of the mts-1 protein (SEQ ID NO:4):  
Ala-Cys-Pro-Leu-Glu-Lys-Ala-Leu-Asp-Val;
- 10 2) Peptide encoding the calcium binding domain of the mts-1 protein (amino acids 22-37, SEQ ID NO:5):  
Lys-Glu-Gly-Asp-Lys-Phe-Lys-Leu-Asn-Lys-Ser-Glu-Leu-Lys-Glu-Leu;
- 15 3) Unique peptide encoding amino acids 42-54 of the mts-1 protein (SEQ ID NO:6):  
Leu-Pro-Ser-Phe-Leu-Gly-Lys-Arg-Thr-Asp-Glu-Ala-Ala;
- 20 4) Unique peptide encoding amino acids 87-101 of mts-1 protein (SEQ ID NO:7):  
Asn-Glu-Phe-Phe-Glu-Gly-Phe-Pro-Asp-Lys-Gln-Pro-Arg-Lys-Lys.

25

Polyclonal antibodies directed against the mts-1 protein are prepared by injection of a suitable laboratory animal with an effective amount of the peptide or antigenic component, collecting serum from the animal, and isolating specific sera by any of the known immunoadsorbent techniques. Animals which can readily be used for producing polyclonal anti-mts-1 antibodies include chickens, mice, rabbits, rats, goats, horses and

30

the like. Chickens are preferred because a better immune response can be obtained and because antibodies can be collected from eggs rather than by bleeding. Although the polyclonal antibodies produced by this method are  
5 utilizable in virtually any type of immunoassay, they are generally less favored because of the potential heterogeneity of the product.

The use of monoclonal antibodies in the diagnostic or detection assays of the present invention  
10 is particularly preferred because large quantities of antibodies, all of similar reactivity, may be produced. The preparation of hybridoma cell lines for monoclonal antibody production is done by fusing an immortal cell line and the antibody producing lymphocytes. This can be  
15 done by techniques which are well known to those who are skilled in the art. (See, for example, Harlow, E. and Lane, D., Antibodies: A Laboratory Manual, Cold Spring Harbor Press, 1988; or Douillard, J. Y. and Hoffman, T., "Basic Facts About Hybridomas", in Compendium of  
20 Immunology Vol. II, L. Schwartz (Ed.), 1981.

Unlike the preparation of polyclonal sera, the choice of animal for monoclonal antibody preparation is dependent on the availability of appropriate immortal cell lines capable of fusing with the monoclonal antibody  
25 producing lymphocytes derived from the immunized animal. Mouse and rat have been the animals of choice for hybridoma technology and are preferably used. Humans can also be utilized as sources for antibody producing lymphocytes if appropriate immortalized human (or  
30 nonhuman) cell lines are available. For the purpose of making the monoclonal antibodies of the present invention, the animal of choice may be injected with from

about 0.01 mg to about 20 mg of the purified mts-1 antigen. Usually the injecting material is emulsified in Freund's complete adjuvant. Boosting injections are generally also required. The separate immortalized cell lines obtained by cell fusion may be tested for antibody production by testing the cell culture media for the ability to find the appropriate antigen.

Lymphocytes can be obtained by removing the spleen or lymph nodes of immunized animals in a sterile fashion. Alternately, lymphocytes can be stimulated or immunized in vitro, as described, for example, in C. Reading J. Immunol. Meth. 53:261-291 1982. To immortalize the monoclonal antibody producing lymphocytes, the lymphocytes must be fused to immortalized cells. A number of cell lines suitable for fusion have been developed, and the choice of any particular line for hybridization protocols is directed by any one of a number of criteria such as speed, uniformity of growth characteristics, deficiency of its metabolism for a component of the growth medium, and potential for good fusion frequency. Intraspecies hybrids, particularly between like strains, work better than interspecies fusions.

Several cell lines are available, including mutants selected for the loss of ability to create myeloma immunoglobulin. Included among these are the following mouse myeloma lines: MPC<sub>11</sub> -X45-6TG, P3 NS1/1-Ag4-1, P3-X63-Ag14 (all BALB/C derived), Y3'Ag1.2.3 (rat), and U266 (human).

Cell fusion can be induced either by virus, such as Epstein-Barr or Sendai virus, or polyethylene glycol. Polyethylene glycol (PEG) is the most efficacious agent for the fusion of mammalian somatic cells. PEG

itself may be toxic for cells, and various concentrations should be tested for effects on viability before attempting fusion. The molecular weight range of PEG may be varied from 1,000 to 6,000. It give best results when diluted to from about 20% to about 70% w/w in saline or serum-free medium. Exposure to PEG at 37°C for about 30 seconds is preferred in the present case, utilizing murine cells. Extremes of temperature (i.e. about 45°C) are avoided, and preincubation of each component of the fusion system at 37°C prior to fusion gives optimum results. The ratio between lymphocytes and immortalized cells optimized to avoid cell fusion amongst lymphocytes ranges of from about 1:1 to about 1:10. .

The successfully fused cells can be separated from the immortalized cell line by any technique known by the art. The most common and preferred method is to choose an immortalized cell line which is Hypoxanthine Guanine Phosphoribosyl Transferase (HGPRT) deficient. Since these cells will not grow in an aminopterin-containing medium, only hybrids of lymphocytes and immortalized cells will grow. The aminopterin-containing medium is generally composed of hypoxanthine  $1 \times 10^{-4}$  M, aminopterin  $1 \times 10^{-5}$  M, and thymidine  $3 \times 10^{-5}$  M, commonly known as the HAT medium. Fused cells are generally grown for two weeks and then fed with either regular culture medium or hypoxanthine, thymidine- containing medium.

The fused cell colonies are then tested for the presence of antibodies that recognize the mts-1 protein. Detection of hybridoma antibodies can be performed using an assay where the antigen is bound to a solid support

and allowed to react to hybridoma supernatants containing putative antibodies. The presence of antibodies may be detected by "sandwich" techniques using a variety of indicators. Most of the common methods are sufficiently sensitive for use in the range of antibody concentrations secreted during hybrid growth.

Cloning of hybrid cells can be carried out after 20-25 days of cell growth in selected medium. Cloning can be performed by cell limiting dilution in fluid phase or by directly selecting single cells growing in semi-solid agarose. For limiting dilution, cell suspensions are diluted serially to yield a statistical probability of having only one cell per well. For the agarose techniques, hybrids are seeded in a semisolid upper layer, over a lower layer containing feeder cells. The colonies from the upper layer may be picked up and eventually transferred to wells.

Antibody-secreting hybrid cells can be grown in various tissue culture flasks, yielding supernatants with variable concentrations of antibodies. In order to obtain higher concentrations, hybrid cells may be transferred into animals to obtain inflammatory ascites. Antibody-containing ascites can be harvested 8-12 days after intraperitoneal injection. The ascites contain a higher concentration of antibodies but include both monoclonals and immunoglobulins from the inflammatory ascites. Antibody purification may then be achieved by, for example, affinity chromatography.

One embodiment of the present invention is directed to a method for diagnosing metastatic cancer by contacting or applying an antibody reactive with an mts-1 polypeptide to a tissue or blood sample taken from an

individual to be tested for metastatic cancer. Formation of an antigen-antibody complex in this immunoassay is diagnostic of metastatic cancer.

In a preferred embodiment, the present invention provides a method for diagnosing metastatic cancer which involves contacting serum from an individual to be tested for such cancer with an antibody reactive with a mammalian mts-1 protein or an antigenic fragment thereof, for a time and under conditions sufficient to form an antigen-antibody complex, and detecting the antigen-antibody complex.

The presence of the mts-1 protein, or its antigenic components, in a patient's serum, tissue or biopsy sample can be detected utilizing antibodies prepared as above, either monoclonal or polyclonal, in virtually any type of immunoassay. A wide range of immunoassay techniques are available as can be seen by reference to Harlow, et al. (Antibodies: A Laboratory Manual, Cold Spring Harbor Press, 1988) and U.S. Pat. Nos. 4,016,043 and 4,424,279. This, of course, includes both single-site and two-site, or "sandwich" of the non-competitive types, as well as in traditional competitive binding assays. Sandwich assays are among the most useful and commonly used assays. A number of variations of the sandwich assay technique exist, and all are intended to be encompassed by the present invention. Briefly, in a typical forward assay, an unlabeled antibody is immobilized in a solid substrate and the sample to be tested brought into contact with the bound molecule. After a suitable period of incubation, for a period of time sufficient to allow formation of an antibody-antigen binary complex, a second antibody,

labeled with a reporter molecule capable of producing a detectable signal is then added and incubated, allowing tie sufficient for the formation of a ternary complex of antibody-labeled antibody. Any reacted material is washing way, and the presence of the antigen is determined by observation of a signal produced by the reporter molecule. The results may either be qualitative, by simple observation of the visible signal, or may be quantitated by comparing with a control sample containing known amounts of hapten. Variations on the forward assay include a simultaneous assay, in which both sample and labeled antibody are added simultaneously to the bound antibody, or a reverse assay in which the labeled antibody and sample to be tested are first combined, incubated and then added to the unlabeled surface bound antibody. These techniques are well known to those skilled in the art, and then possibly of minor variations will be readily apparent. As used herein, "sandwich assay" is intended to encompass all variations on the basic two-site technique.

The mts-1 protein may also be detected by a competitive binding assay in which a limiting amount of antibody specific for the mts-1 protein is combined with specified volumes of samples containing an unknown amounts of the mts-1 protein and a solution containing a detectably labeled known amount of the mts-1 protein. Labeled and unlabeled molecules then compete for the available binding sites on the antibody. Phase separation of the free and antibody-bound molecules allows measurement of the amount of label present in each phase, thus indicating the amount of antigen or hapten in the

sample being tested. A number of variations in this general competitive binding assays currently exist.

In any of the known immunoassays, for practical purposes, one of the antibodies or the antigen will be typically bound to a solid phase and a second molecule, either the second antibody in a sandwich assay, or, in a competitive assay, the known amount of antigen, will bear a detectable label or reporter molecule in order to allow visual detection of an antibody-antigen reaction. When two antibodies are employed, as in the sandwich assay, it is only necessary that one of the antibodies be specific for the mts-1 protein or its antigenic components. The following description will relate to a discussion of a typical forward sandwich assay; however, the general techniques are to be understood as being applicable to any of the contemplated immunoassays.

In the typical forward sandwich assay, a first antibody having specificity for the mts-1 protein or its antigenic components is either covalently or passively bound to a solid surface. The solid surface is typically glass or a polymer, the most commonly used polymers being cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene. The solid supports may be in the form of tubes, beads, discs or microplates, or any other surface suitable for conducting an immunoassay. The binding processes are well-known in the art and generally consist of cross-linking covalently binding or physically adsorbing the molecule to the insoluble carrier. Following binding, the polymer-antibody complex is washed in preparation for the test sample. An aliquot of the sample to be tested is then added to the solid phase complex and incubated at a suitable temperature ranging



from about 4°C. to about 37°C (for example 25°C) for a period of time sufficient to allow binding of any subunit present in the antibody. The incubation period will vary but will generally be in the range of about 2-40 minutes to several hours. Following the incubation period, the antibody subunit solid phase is washed and dried and incubated with a second antibody specific for a portion of a mts-1 hapten. The second antibody is linked to a reporter molecule which is used to indicate the binding of the second antibody to the hapten.

By "reporter molecule", as used in the present specification and claims, is meant a molecule which, by its chemical nature, provides an analytically identifiable signal which allows the detection of antigen-bound antibody. Detection may be either qualitative or quantitative. The most commonly used reporter molecules in this type of assay are either enzymes, fluorophores or radionuclide containing molecules. In the case of an enzyme immunoassay, an enzyme is conjugated to the second antibody, generally by means of glutaraldehyde or periodate. As will be readily recognized, however, a wide variety of different conjugation techniques exist, which are readily available to the skilled artisan. Commonly used enzymes include horseradish peroxidase, glucose oxidase,  $\beta$ -galactosidase and alkaline phosphates, among others. The substrates to be used with the specific enzymes are generally chosen for the production, upon hydrolysis by the corresponding enzyme, of a detectable color change. For example, p-nitrophenyl phosphate is suitable for use with alkaline phosphatase conjugates; for peroxidase conjugates,

1,2-phenylenediamine, 5-aminosalicylic acid, or toluidine are commonly used. It is also possible to employ fluorogenic substrates, which yield a fluorescent product rather than the chromogenic substrates noted above. In all cases, the enzyme-labeled antibody is added to the first antibody hapten complex, allowed to bind, and then the excess reagent is washed away. A solution containing the appropriate substrate is then added to the ternary complex of antibody-antigen-antibody. The substrate will react with the enzyme linked to the second antibody, giving a qualitative visual signal, which may be further quantitated, usually spectrophotometrically, to give an indication of the amount of hapten which was present in the sample.

Alternately, fluorescent compounds, such as fluorescein and rhodamine, may be chemically coupled to antibodies without altering their binding capacity. When activated by illumination with light of a particular wavelength, the fluorochrome-labeled antibody absorbs the light energy, inducing a state of excitability in the molecule, followed by emission of the light at a characteristic color visually detectable with a light microscope. The fluorescent labeled antibody is allowed to bind to the first antibody-hapten complex. After washing off the unbound reagent, the remaining ternary complex is then exposed to the light of the appropriate wavelength, the fluorescence observed indicates the presence of the hapten of interest. Immunofluorescence techniques are very well established in the art. However, other reporter molecules, such as radioisotope, chemiluminescent or bioluminescent molecules, may also be employed. It will be readily apparent to the skilled

technician how to vary the procedure to suit the required purpose.

In another embodiment, the antibodies directed against the mts-1 protein may be incorporated into a kit for the detection of the mts-1 protein. Such a kit may encompass any of the detection systems contemplated and described herein, and may employ either polyclonal or monoclonal antibodies directed against the mts-1 protein. Both mts-1 antibodies complexed to a solid surface described above or soluble mts-1 antibodies are contemplated for use in a detection kit. A kit of the present invention has at least one container having an antibody reactive with a mammalian mts-1 polypeptide. However, the present kits can have other components. For example, the kit can be compartmentalized: the first container contains mts-1 protein as a solution, or bound to a solid surface, to act as a standard or positive control, the second container contains anti-mts-1 primary antibodies either free in solution or bound to a solid surface, a third container contains a solution of secondary antibodies covalently bound to a reporter molecule which are reactive against either the primary antibodies or against a portion of the mts-1 protein not reactive with the primary antibody. A fourth and fifth container contains a substrate, or reagent, appropriate for visualization of the reporter molecule.

The subject invention therefore encompasses polyclonal and monoclonal antibodies useful for the detection of mts-1 protein as a means of diagnosing metastatic cancer. Said antibodies may be prepared as described above, then purified, and the detection systems contemplated and described

herein employed to implement the subject invention.

The present invention also contemplates treating metastatic cancers and tumors by inactivating, destroying or nullifying the mts-1 gene or protein, or cells expressing the mts-1 gene. The treatment of cancer, as described in the specification and claims, contemplates preferably lung, liver, kidney, thyroid, mammary gland, leukemic, pancreatic, endometrial, ovarian, cervical, skin, colon or lymphoid cancers. For example, the antibodies, prepared as described above, may be utilized to inactivate mts-1 protein expressing cells: either unconjugated anti-mts-1 antibodies or anti-mts-1 antibodies conjugated to a toxin may be employed in the therapy of cancer.

Moreover, the present invention provides a method of inhibiting metastasis in a cancerous cell by providing to the cancerous cell a nucleic acid encoding an antisense mts-1 nucleotide sequence. For example, such an antisense nucleic acid can have at least 10 nucleotides of the antisense strand of SEQ ID NO:1 or SEQ ID NO:3. Preferably, the antisense mts-1 nucleic acids of the present invention have at least 15 or 17 nucleotides.

In one embodiment, this method employs an expression vector including a nucleic acid encoding an antisense nucleotide sequence for mts-1 operably linked to a segment of the vector which can effect expression of an antisense mts-1 RNA. Any of the foregoing expression vectors which can express high levels of mts-1 RNA can be used for this method including, e.g., pTrcHis.

According to the present invention, antisense mts-1 nucleic acids can inhibit metastatic cancer by

binding to sense mts-1 mRNA. Such binding can either prevent translation of mts-1 protein or destroy mts-1 sense mRNA, e.g., through the action of RNaseH. Accordingly, less mts-1 protein is available to potential metastatic tumor cells and metastasis of these cells is prevented.

Another embodiment of the present invention contemplates pharmaceutical compositions containing, for example, an antibody reactive with a mammalian mts-1 polypeptide, an antisense mts-1 nucleic acid or the mts-1 protein. The mts-1 protein is known to bind calcium and has a role in the growth of cells (Linzer, et al., Proc. Natl. Acad. Sci. USA 80:4271-4275, 1983; Jackson-Grusby, et al., Nuc. Acids. Res. 15:6677-6689; Goto et al., J. Biochem. 103:48-53, 1988). The mts-1 protein is also very closely related to 42A, a gene thought to have a role in nerve cell growth (Masiakowski, et al. Proc. Natl. Acad. Sci. USA 85:1277-1281, 1988). The mts-1 protein may also have a role in the differentiation of myoepithelial cells (Barracough, et al., J. Mol. Biol. 198:13-20, 1987). Hence the human mts-1 protein may be clinically useful, for example, in stimulating cells in general or preferably, nerve cells, to grow, and further, in promoting the differentiation of myoepithelial cells.

The active ingredients of a pharmaceutical composition containing the mts-1 protein or anti-mts-1 antibodies and antisense mts-1 nucleic acids (i.e. anti-cancer reagents) are contemplated to exhibit effective therapeutic activity, for example, in promoting cell growth, or for treating cancer, respectively. Thus the active ingredients of the therapeutic compositions containing mts-1 protein cell proliferative activity or

anti-cancer reagents, are administered in therapeutic amounts which depend on the particular disease. For example, from about 0.5  $\mu$ g to about 2000 mg per kilogram of body weight per day may be administered. The dosage regimen may be adjusted to provide the optimum therapeutic response. For example, several divided doses may be administered daily or the dose may be proportionally reduced as indicated by the exigencies of the therapeutic situation. A decided practical advantage is that the active compound may be administered in a convenient manner such as by the oral, intravenous (where water soluble), intramuscular, subcutaneous, intranasal, intradermal or suppository routes. Depending on the route of administration, the active ingredients which comprise mts-1 proteins or anti-cancer reagents may be required to be coated in a material to protect said ingredients from the action of enzymes, acids and other natural conditions which may inactivate said ingredients. For example, the low lipophilicity of mts-1 protein, and some anti-cancer reagents, may allow them to be destroyed in the gastrointestinal tract by enzymes capable of cleaving peptide or nucleotide bonds and in the stomach by acid hydrolysis. In order to administer mts-1 protein or anti-cancer reagents by other than parenteral administration, they should be coated by, or administered with, a material to prevent its inactivation. For example, mts-1 protein or anti-cancer reagents may be administered in an adjuvant, co-administered with enzyme inhibitors or in liposomes. Adjuvants contemplated herein include resorcinols, non-ionic surfactants such as polyoxyethylene oleyl ether and n-hexadecyl polyethylene ether. Enzyme inhibitors include pancreatic trypsin

inhibitor, diisopropylfluorophosphate (DFP) and trasylol. Liposomes include water-in-oil-in-water P40 emulsions as well as conventional liposomes.

5 The active compounds may also be administered parenterally or intraperitoneally. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof, and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

10 The pharmaceutical forms suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. In all cases the form must be  
15 sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier  
20 can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, liquid polyethylene glycol, and the like), suitable mixtures thereof and vegetable oils. The proper fluidity can be maintained, for example, by the  
25 use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. The preventions of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example,  
30 parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases it will be preferable to include isotonic agents, for example,

sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

5 Sterile injectable solutions are prepared by incorporating the active compounds in the required amount in the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are  
10 prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable  
15 solutions, the preferred methods of preparation are vacuum-drying and the freeze-drying technique which yield a powder of the active ingredient plus any additional desired ingredient from previously sterile-filtered solution thereof.

20 When the mts-1 protein or anti-cancer reagents are suitably protected as described above, the active compound may be orally administered, for example, with an inert diluent or with an assimilable edible carrier, or it may be enclosed in hard or soft shell gelatin capsule,  
25 or it may be compressed into tablets, or it may be incorporated directly with the food of the diet. For oral therapeutic administration, the active compound may be incorporated with excipients and used in the form of ingestible tablets, buccal tablets, troches, capsules,  
30 elixirs, suspensions, syrups, wafers, and the like. Compositions or preparations according to the present invention are prepared so that an oral dosage unit form



contains between about 0.5 µg and 2000 µg of active compound.

5 The tablets, troches, pills, capsules, and the like, as described above, may also contain the following:  
a binder such as gum tragacanth, acacia, corn starch or gelatin; excipients such as dicalcium phosphate; a  
10 disintegrating agent such as corn starch, potato starch, alginic acid, and the like; a lubricant such as magnesium stearate; and a sweetening agent such as sucrose, lactose or saccharin may be added or a flavoring agent such as  
peppermint, oil of wintergreen or cherry flavoring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid  
15 carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills or capsules may be coated with shellac, sugar or both. A syrup or elixir may contain the active compound, sucrose as a sweetening agent, methyl and propylparabens as preservatives, a dye  
20 and flavoring such as cherry or orange flavor. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compound may be incorporated into  
25 sustained-release preparations and formulations.

It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited  
30 as unitary dosages for the mammalian subjects to be treated; each unit containing a predetermined quantity of the active material calculated to produce the desired

therapeutic effect in association with the required pharmaceutical carrier. The specification for the novel dosage unit forms of the invention are dictated by and directly depending on (a) the unique characteristics of the active material and the particular therapeutic effect to be achieved, and (b) the limitations inherent in the art of compounding such as active material for the treatment of disease in living subjects having a diseased condition in which bodily health is impaired as herein disclosed in detail.

The principal active ingredient is compounded for convenient and effective administration in effective amounts with a suitable pharmaceutically acceptable carrier in dosage unit form as hereinbefore disclosed. A unit dosage form can, for example, contain the principal active compound in amounts ranging from 0.5  $\mu$ g to about 2000  $\mu$ g. Expressed in proportions, the active compound is generally present in from about 10 .mu.g to about 2000 mg/ml of carrier. In the case of compositions containing supplementary active ingredients, the dosages are determined by reference to the usual dose and manner of administration of the said ingredients.

As used herein "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and adsorption delaying agents, and the like. The use of such media gents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, use thereof in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

The present invention is further directed to treating tumors by interfering with, destroying or nullifying the function of mts-1 gene or protein.

In accordance with the present invention, Mts-1  
5 interferes with the function of tumor suppressor p53 by binding to p53. The present inventors have demonstrated that binding with Mts-1 inhibits p53 phosphorylation by PKC, represses the DNA-binding activity of p53 and reduces the transactivation capacity of p53. The present  
10 invention has further identified that the Mts-1 protein binds to the C-terminal region of p53. Accordingly, the present invention provides compositions and methods useful for treating tumors by interfering with the expression or function of Mts-1, e.g., intercepting the  
15 interaction between Mts-1 and tumor suppressor p53.

The present invention provides peptides which prevent p53 from binding to Mts1, e.g., a peptide comprising aa 289-393 of human p53, a peptide comprising  
20 aa 360-393 of human p53, a peptide comprising aa 289-390 of murine p53, a peptide comprising aa 360-390 of murine p53, a peptide comprising the C-terminal nonmuscle myosin heavy chain, a peptide comprising amino acid 1909-1937 of human nonmuscle myosin heavy chain. Functional fragments and analogs of these peptides are also contemplated by  
25 the present invention.

"Functional fragments" refer to peptide  
fragments that have the same function as the peptide in  
issue, namely, the function of interfering the Mts1-p53  
interaction by binding to Mts-1.  
30

By "analogs" it means variants of a peptide in issue. The variations include substitutions, insertions or deletions of one or more amino acid residues, or modifications of the side chains of the amino acid residues. Thus, analogs of a peptide can include homologous peptides from other mammalian species, peptides containing non-natural amino acid residues, peptides having chemical modifications on the side groups of amino acid residues, as well as peptides artificially designed to resemble the three dimensional structure of the binding site on human p53.

A variety of techniques are available to those skilled in the art to make various fragments or analogs of p53. Such techniques include standard chemical synthesis, recombinant expression, and structural modeling (also called 'mimetics'). The sequences of p53 from a number of mammalian species are highly conserved and are available to those skilled in the art, e.g., via Databases such as GenBank.

Mimetics is a well-known technique involving the design of compounds which contain functional groups arranged in a manner mimicking that of the original, lead compound. Mimetics is desirable where the synthesis of the original compound is difficult, or where the original compound is unsuitable for a particular method of administration (e.g., orally) as such compound may tend to be degraded too quickly by proteases in the alimentary canal. Mimetic design, synthesis and testing can avoid laborious screenings of a large number of molecules for a target property.

5 A variety of methods can be employed to  
determine whether a fragment or analog is "functional",  
i.e., capable of interfering the interaction between Mts-  
1 and p53 by binding to Mts-1. In one format, for  
example, a sample containing Mts-1 proteins can be  
contacted with a test compound for a period of time  
sufficient to allow binding of the test compound to Mts-  
1. Then, the sample is contacted with p53, and the  
amount of complexes formed between Mts-1 and p53 can be  
10 measured and compared to the amount of complexes formed  
in the absence of the test compound. A decrease in the  
value determines the test compound as a compound which  
prevents the binding of Mts-1 to p53.

15 An alternative format to carry out the method  
of the present invention can include as a first step,  
contacting a sample containing Mts-1 with p53 for a time  
sufficient to allow p53 to bind to Mts-1 and measuring  
the amount of complexes formed between Mts-1 and p53 in  
the sample. Afterwards, the sample is contacted with a  
20 test compound for an appropriate period of time.  
Compounds which displace p53 from the prior formed p53-  
Mts1 complexes can be identified as a compound which  
prevents the binding of Mts-1 to p53.

25 A variety of biochemical assays and  
immunoassays can be employed for measuring the amount of  
the Mts1-p53 complexes formed in a sample. The proteins  
can be conveniently labeled with, e.g., isotope, biotinyl  
group, or fluorescein, to facilitate the detection. The  
assays can be carried out in a variety of formats, such  
30 as immunoprecipitation, Far Western blot analysis, RIA,

ELISA, forward or reverse sandwich assays, peptide competition binding assays, and the like. Peptides identified by using any of the above-described biochemical assays or immunoassays can be further tested and confirmed in functional assays, such as DNA-binding gel shift assay, or a reporter expression assay, which are further described in the Examples hereinafter.

The present invention also contemplates pharmaceutical compositions which include, as an active ingredient, an Mts1-p53 binding intercepting peptide as described hereinabove, and a pharmaceutically acceptable carrier.

In another aspect of the present invention, Mts1-p53 binding-intercepting peptides or nucleic acid molecules encoding thereof are used for treating tumors.

By "treating a tumor" it means that the tumor growth or metastasis is significantly inhibited, as indicated by reduced tumor volume or reduced occurrences of tumor metastasis. Tumor growth can be determined, e.g., by examining the tumor volume via routine procedures (such as obtaining two-dimensional measurements with a dial caliper). Tumor metastasis can be determined by examining the appearance of tumor cells in secondary sites or examining the metastatic potential of biopsied tumor cells in vitro using various laboratory procedures.

According to the present invention, the tumors which can be treated by using the methods of the present invention may include, but are not limited to, melanoma, lymphoma, plasmocytoma, sarcoma, glioma, thymoma,

leukemia, breast cancer, prostate cancer, colon cancer, esophageal cancer, brain cancer, lung cancer, ovary cancer, cervical cancer, hepatoma, and other neoplasms known in the art.

5           The present invention contemplates particularly p53-related tumors. The term "p53-related" refers to tumor cells in which wild-type (wt) p53 is absent, disabled or otherwise mutated.

10           A variety of methods are available to those skilled in the art for determining whether a tumor is "p53-related". For example, EPA 518 650 (Vogelstein, B. et al.) describes a method for detecting p53 in cellular extracts using DNA sequences that are specific for p53 binding. WO 94/11533 describes determining the presence  
15           of functional p53 in cells by measuring mRNA or protein encoded by a growth-arrest and DNA-damage inducible gene, GADD45. U.S. Patent 5,876,711 describes a rapid in vivo method for determining the status of tumor suppressor proteins in patient tumor cells. Such method includes  
20           contacting the tumor cells with a first and second polynucleotide sequence such that they are taken up by the tumor cells. The first polynucleotide sequence encodes a reporter molecule that is operably linked to the second polynucleotide sequence which sequence binds  
25           the tumor suppressor. Binding of the tumor suppressor causes the expression of the reporter molecule, which is then detected or quantitated.

30           In one embodiment, the present invention provides methods of treating a tumor in a subject by administering to the subject, a therapeutically effective

amount of a peptide which prevents the binding of Mts-1 to p53. Preferred binding intercepting peptides have been described hereinabove.

In another embodiment, the present invention provides methods of treating a tumor in a subject by administering to the subject, a therapeutically effective amount of a nucleic acid molecule coding for a peptide which prevents the binding of Mts-1 to p53.

Preferably, such nucleotide sequence is provided in an expression vector. Preferred expression vectors for use in a therapeutic composition include any appropriate gene therapy vectors, such as nonviral (e.g., plasmid vectors), retroviral, adenoviral, herpes simplex viral, adeno-associated viral, polio viruses and vaccinia vectors. Examples of retroviral vectors include, but are not limited to, Moloney murine leukemia virus (MoMuLV), Harvey murine sarcoma virus (HaMuSV), murine mammary tumor virus (MuMTV), and Rous Sarcoma Virus (RSV)-derived recombinant vectors. More preferably, a non-human primate retroviral vector is employed, such as the gibbon ape leukemia virus (GaLV), thereby providing a broader host range than murine vectors, for example. Gene therapy vectors can be made tissue specific by, for example, linking the nucleotide sequence to a tissue-specific promoter. Multiple teachings of gene therapy are available for those skilled in the art, e.g., W.F. Anderson (1984) "Prospects for Human Gene Therapy" *Science* 226: 401-409; S.H. Hughes (1988) "Introduction" *Current Communications in Molecular Biology* 71: 1-12; N. Muzyczka and S. McLaughlin (1988)



"Use of Adeno-associated Virus as a Mammalian Transduction Vector" *Communications in Molecular Biology* 70: 39-44; T. Friedman (1989) "Progress Toward Human Gene Therapy" *Science* 244: 1275-1281 and W.F. Anderson (1992) "Human Gene Therapy" *Science* 256: 608-613.

The nucleic acid molecule can be delivered "naked" by direct injection into the blood stream or to the desired tissue or organ of a subject. Alternatively, the vector can be combined with a lipid compound which facilitates the uptake of the molecule by cells. The lipid compound include liposome, lipofectins, cytofectins, lipid-based positive ions, and then introduced into the body fluids, the blood stream, or a selected tissue site. Liposome mediated gene therapy is well known in the art and is described by, e.g., Lesoon-Wood et al., *Human Gene Ther.* 6: 395, 1995; Tsan et al., *Am. J. Physiol* 268: 11052, 1995; Vieweg et al., *Cancer Res.* 55: 2366, 1995; Trivedi et al., *J. Neurochem.* 64: 2230, 1995; Hickman et al., *Human Gene Ther.* 5: 1477, 1994; Westbrook et al. *Human Mol Genet.* 3: 2005, 1994; Schmid et al., *Z. Gastroenterol* 32: 665, 1994; Hofland et al., *Biochem. Biophys. Res. Commun.* 207: 492, 1995; Plautz et al., *Ann. N.Y. Acad. Sci.* 716: 144, 1994. Other DNA carriers which can facilitate the uptake of a desired vector by the target cells include nuclear protein, or ligands for certain cell receptors, which can be combined with a vector in engineered vesicles for delivery.

In another embodiment, the present invention provides a method of treating a tumor in a subject by

administering to the subject, a therapeutically effective amount of an antibody directed against Mts-1.

The present invention provides, as an example, that the administration of an anti-Mts-1 monoclonal antibody to mice bearing highly metastatic CSML-100 tumors has a significant inhibitory effect on both tumor growth and metastasis.

Both monoclonal and polyclonal antibodies directed against a mammal Mts-1 protein, including rat, mouse and human, can be employed for practicing the methods of the present invention. Such antibodies can be readily generated using the entire Mts-1 protein as an antigen or by using short peptides, encoding portions of the Mts-1 protein, as antigens. Preferably, specific peptides encoding unique portions of the Mts gene are synthesized for use as antigens for obtaining anti-Mts1 antibodies. Those skilled in the art can refer to U.S. Patent 5,801,142 for relevant teachings. The Fab, Fab', F(ab')<sub>2</sub>, fragments of such antibodies, as well as single-chain anti-Mts-1 antibodies can also be employed in the present methods. The antibodies can be either unconjugated anti-mts-1 antibodies or anti-mts-1 antibodies conjugated to a toxin.

In still another embodiment, the present invention provides methods of treating a tumor in a subject by administering a therapeutically effective amount of an antisense DNA of Mts-1 gene.

According to the present invention, antisense mts-1 nucleic acids can inhibit metastatic cancer by binding to sense mts-1 mRNA. Such binding can either

prevent translation of mts-1 protein or destroy mts-1 sense mRNA, e.g., through the action of RNaseH.

An Mts-1 antisense DNA can have at least about 10 nucleotides, preferably, at least about 15 or 17 nucleotides, more preferably, at least about 50 nucleotides. The antisense DNA is preferably inserted into an expression vector in an operable linkage to a promoter which can effect the transcription of the antisense RNA. Any of the foregoing gene therapy vectors can be used for practicing the methods of the present invention.

In practicing the above-described methods of the present invention, the active compound (i.e., the binding-intercepting peptides, the nucleic acid molecules encoding such peptides, anti-Mts1 antibodies, or Mts-1 antisense DNAs) can be used in combination with one another, or with other anti-tumor agents that are available in the art.

Another embodiment of the present invention relates to the animal tumors and tumor cell lines developed in accordance with the present invention which are useful as model systems of the metastatic process. These tumors and cell lines can be utilized for screening anti-metastatic drugs and for developing therapeutic regimens for the treatment of malignant cancer is provided by the present invention. The tumors provided by the present invention include the IR6 and IR4 tumors. The tumor cell lines provided by the present invention include CSML-0, CSML-50, CSML-100, HMC-0, HMC-Lr, T9, T36, LMEC, PCC4c-P, PCC4c-B, PCC4c-107, IR6CL<sub>1</sub>, IR4 CL,

ELCL<sub>1</sub>, TRCL<sub>1</sub> and the murine lung carcinoma Line 1.

5 The tumors or cell lines of the present invention each have a highly predictable metastatic potential; however the metastatic potentials of related, but separate, tumors or cell lines can be very different. The properties, and metastatic potentials, of the tumors and cell lines of the present invention are fully described in Examples 1, 2, 3 and 12 and in Tables 1 and 2. While these tumors and cell lines were derived from mouse mammary carcinomas as well as rat thyroid and epithelial carcinomas, they are useful for the development of a variety of human cancer therapies, for several reasons. First, cancer cells all have similar properties, including, for example, unrestrained growth and lack of contact inhibition, which suggests that the process of cancer development is similar in all cancers. Second, the morphologies and biochemical properties of the tumors developed after injection of these tumor-derived cells are identical to analogous tumors in humans. Hence, potential anti-cancer therapies or drugs may effectively be screened by employing the animal model system of the current invention.

25 The utility of these unique tumors and cell lines is apparent to one skilled in the art. Briefly, animals are injected with tumors or tumor-derived cells which have a predictable metastatic potential. A proportion of the animals are treated with a potential anti-cancer drug or therapy. After a suitable period of time, all animals are sacrificed and the tissues of both treated and non-treated animals are examined for the development of primary and secondary (metastatic) tumors.

If a therapeutic regimen is successful, the 1 treated animals should have a much lower incidence of tumor formation.

Both mouse and rat model systems are provided by the present invention for the development of cancer therapy. A spontaneous mouse mammary carcinoma has been used to generate different cell lines with low, intermediate and high incidences of metastasis. This is done by intramuscular transplantation or subcutaneous tail transplantations of the original spontaneous mammary tumor cells into syngeneic mice. Intramuscular transplantation has yielded a cell line called CSML-0 which has low metastatic potential. Solitary lung metastasis are detected in less than 10% of CSML-0 injected animals sacrificed because of a moribund condition. The highly metastatic CSML-100 cell line has been generated by selection of the metastatic phenotype through successive subcutaneous transplantations of CSML metastatic cells into the tail. The CSML-50 cell line, selected during the generation of CSML-100, has an intermediate level of metastatic potential.

A variety of rat tumors have been generated by irradiating normal Fischer 344 rat thyroid cell suspensions and then transplanting these cells into rats. Grafts of non-irradiated thyroid cells develop into morphologically and functionally normal thyroid tissue after transplantation into Fischer 344 syngenic rats, if elevated levels of thyroid stimulating hormone are also provided. Irradiation of thyroid cell suspensions before transplantation has produced a series of rat thyroid carcinomas which are histopathologically identical to human counterparts. For example, the IR6 tumor, generated

in accordance with the present invention, is highly metastatic, while the IR4 tumor has low metastatic potential. Both tumors are structurally and histologically identical to corresponding human tumors (FIG. 7).

The extensive variety of tumors and cell lines, and the varying metastatic potential of these tumors and cell lines, provides mouse and rat model systems amenable to carefully controlled studies directed towards the dissection of the metastatic process. Therapeutic regimens for treatment of malignant cancer can be developed by controlled studies of groups of animals injected with cells of high, low and intermediate metastatic potential. A drug, or pharmaceutical composition suspected of having anti-metastatic potential, may be used to treat a proportion of animals from each group. The incidence of metastasis amongst the animals receiving the drug or pharmaceutical composition may be compared with the incidence amongst animals not receiving treatment. Therefore, the present invention provides an animal system for distinguishing effective anti-metastatic drugs and therapies from those that are ineffective.

The Examples serve to further illustrate the invention without in any way limiting same.

## EXAMPLE 1

### Materials And Methods

#### 5 1. Medium

Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal calf serum (FCS) was used for all cell lines. Cells were passed weekly.

#### 10 2. Metastatic activity

Metastatic activity was determined by intramuscular injection of  $1 \times 10^4$  to  $1 \times 10^6$  tumor cells per tumor cell line in 10-15 mice. Either A/Sn or A/J mice were used.

For A/Sn mice, cultured tumor cells were  
15 trypsinized, rinsed and suspended in sterile Hanks' salt solution. A total of  $1 \times 10^6$  cells in 0.3 ml of Hanks' solution was injected subcutaneously into each 8 to 10 week old A/Sn mouse. The mice were killed 4-5 weeks after tumor inoculation and the number of lung metastasis  
20 was counted. Non-metastatic cell lines were defined as cell lines that did not result in visible metastases. Highly metastatic lines under the same conditions gave rise to multiple metastases in target organs of each  
mouse.

25 Female A/J mice (4-6 weeks old) were injected either with  $1 \times 10^4$  cells intravenously through the tail vein or with  $1 \times 10^6$  cells subcutaneously into the abdomen. Fifteen days following intravenous injection and  
30 4-6 weeks after subcutaneous injection, the animals were sacrificed and the lung metastases were counted.

### 3. Mouse Tumor Cell Lines

CSML-0, CSML-50 and CSML-100 tumor cell lines were established in accordance with the present invention from spontaneous mammary adenocarcinomas of A/Sn mice. These cell lines are described in more detail in Example 2.

HMC-0 and HMV-Lr are tumor cell lines which were also established from spontaneous mammary adenocarcinomas of A/Sn mice. T-9, as well as T-36 and its variant LMEC, are coupled sublines of two original tumors which were induced by ectopic transplantation of 6-7 day-old gestation syngeneic embryos to CBA/J and A/Sn mice.

Cell lines, PCC4c-P, PCC4,-B and PCC4c-107 were derived from PCC4-Blangy, PCC4-Pasteur and PCC4-107 teratocarcinomas, respectively.

A murine lung carcinoma, Line 1, cell line is highly metastatic, however when Line 1 cells are grown in the presence of the 3% DMSO, these cells lose their metastatic potential.

Some of the properties of the above cell lines, and their metastatic potential, are described in Table 1.



TABLE 1  
Metastatic Potential of Analyzed  
Mouse Tumors and Mouse Tumor Cell Lines

5

	Tumors and Cell Lines <sup>a</sup>	Spontaneous Metastases	Target Organs
10	Mammary carcinosarcoma CSML-0 CSML-50 CSML-100	low metastatic <sup>b</sup> 50% high metastatic <sup>c</sup>	lung lung lung
15	Mammary Solid Carcinoma HMC-0 HMC-Lr	low metastatic high metastatic	liver <sup>d</sup> liver <sup>d</sup>
20	Teratocarcinoma cell line PCC4 <sub>c</sub> -B PCC4 <sub>c</sub> -P PCC4 <sub>c</sub> -107 C12 <sub>c</sub>	nonmetastatic nonmetastatic nonmetastatic nonmetastatic	----- ----- ----- -----
25	Embryocarcinoma, T-36 node Cell line derived from T-36, T-36 <sub>c</sub> node Embryocarcinoma, LMEV node Teratocarcinoma, T-9 node	50%  50% high metastatic low metastatic	lymph  lymph lymph
30	Colon Adenocarcinoma, Acatol Melanoma, B-16 Lung carcinoma, RL-67 Lewis lung carcinoma, LLC	nonmetastatic low metastatic high metastatic high metastatic	----- lung lung <sup>d</sup> lung
35	Murine lung carcinoma cell Line 1: Grown without DMSO Grown with 3% DMSO	  high metastatic nonmetastatic	

40

<sup>a</sup> PCC4<sub>c</sub>-B, PCC4<sub>c</sub>-P, and PCC4<sub>c</sub>-107 are cell lines derived from PCC4-Blangy, PCC4-Pasteur, and PCC4-107 teratocarcinomas.

45

<sup>b</sup> Low metastatic indicates 20% of injected mice give rise to solitary metastases.

<sup>c</sup> High metastatic indicates 100% of multiple metastases in target organs.

<sup>d</sup> Metastases in other organs.

5

### 3. Rat Tumors and Rat Tumor Cell Lines

An established epithelial cell line, FRTL5, was derived from a culture of rat thyroid cells and is not tumorigenic. In accordance with the present invention, two tumorigenic but non-metastatic derivatives of FRTL5 cells, ELCL.sub.1 and TRCL.sub.1, have also been isolated. The properties of these non-metastatic cell lines are further elaborated upon in Table 2 and in Example 3.

The IR6 tumor is a radiation induced, transplantable anaplastic thyroid carcinoma, of epithelial origin. It is a poorly differentiated, highly aggressive adenocarcinoma which is highly metastatic. IR4 is another transplantable, radiation induced thyroid tumor which is moderately differentiated and has low metastatic potential. The properties of these tumors are further elaborated on in Example 3 and in Table 2.

### 25 4. Nucleic Acid Purification and Analysis

Tumor cells were cultivated and prepared for subcutaneous injection into mice as described under the metastatic activity subsection of this section. Injected mice were examined weekly for the appearance of tumors. Tumors were excised and used for DNA and RNA preparations. Total DNA was prepared from cells according

to Sambrook et al. (Molecular Cloning: A Laboratory Manual. Cold Spring Harbor, Vol. 2, Laboratory Press, 1989. Pages 9.1-9.62).

5 RNAs were prepared from different tumor cells and normal cells according to the procedure described by Chomczynski et al. (1987, Anal. Biochem. 162: 156-159) or Sambrook et al. (Molecular Cloning: A Laboratory Manual, Vol. 1, Cold Spring Harbor Press, 1989:7.1-7.87). Gel electrophoresis of RNA, RNA blotting to nylon membrane filters, and hybridization with nick-translated DNA probes was as described in Grigorian et al. (1985, EMBO J. 4: 2209-2215).

10 Southern blots were performed using 10 .mu.g of genomic DNA extracted from mouse liver, CSML-100 cells, human placenta and liver, rat liver, pig liver, and chicken liver. DNAs were digested with BamHI, EcoRI, and PstI endonucleases. Following electrophoresis in a 0.8% agarose gel, the DNA was transferred onto a nylon membrane (Hybond N, Amersham). The filter was prehybridized and hybridized following the standard procedure of Sambrook et al., supra.

## EXAMPLE 2

### Development of Benign and Metastatic Mouse Tumor Cell Lines

5 CSML-0, CSML-50 and CSML-100 are tumor lines  
established from spontaneous mammary adenocarcinomas of  
A/Sn mice. CSML-0 was derived from a tumor maintained by  
intramuscular passages and was characterized as having a  
10 low metastatic potential. Solitary lung metastases were  
detected in less than 10% of autopsied animals that had  
been killed because of a moribund condition. A second,  
highly metastatic subline, CSML-100, was developed by  
selecting for a metastatic phenotype in successive  
15 transplantations (via successive subcutaneous tail  
injections) of initially rare, and subsequently more  
frequent, CSML metastatic tumor cells. The frequency of  
metastasis to the lung by CSML-100 cells was 100%, by any  
route of primary inoculation. CSML-50 represents a cell  
20 line with an intermediate level of metastatic potential  
which was developed during the establishment of CSML-100.  
The frequency of lung metastasis by CSML-50 cells was  
about 50%.

25 The CSML-100 tumor line also caused tumors to  
form in A/J mice (Jackson laboratories) which have a  
similar genotype to that of A/Sn mice. CSML cells were  
not rejected by A/J mice and metastases were detected in  
lungs and other organs by any injection route.

30 A/J mice intravenously injected with CSML-100  
developed tumors within 6-7 days of injection. Even when  
only  $1 \times 10^4$  CSML-100 cells were injected, abundant  
metastases were found in lungs by 15 days post-injection  
(FIG. 9c). A/J mice injected with CSML-100 cells by the

subcutaneous route had approximately 250 spontaneous metastases per lung 4-6 weeks later (FIG: 9d). Mice injected with CSML-0 by either route of injection had only 10-25 tumors per lung (FIGS. 9a and 9b). After sacrifice of each mouse, the ovaries, liver, kidney, gonads, muscle, and brain tissues were preserved for immunohistochemical analysis. Such analysis indicated mts-1 was highly expressed in metastasized tumors, particularly in the ovarian and lung tumors.

### EXAMPLE 3

#### Development of Benign and Metastatic Rat Tumors and Rat Tumor Cell Lines

5 A number of rat thyroid carcinomas and cell  
lines have been developed in conjunction with the present  
invention, by irradiating normal Fischer 344 rat thyroid  
cell suspensions before transplantation into the rat.  
10 Grafts of non-irradiated, monodispersed rat thyroid cells  
develop into morphologically and functionally normal  
thyroid tissue within a short time after transplantation  
into Fischer 344 syngeneic rats, if the level of thyroid  
stimulating hormone (TSH) within the rat is elevated by  
15 injection of TSH. If thyroid cells are irradiated before  
transplantation, thyroid carcinomas develop. The IR6  
tumor was obtained as a radiation induced, transplantable  
anaplastic thyroid carcinoma of epithelial origin. IR6  
was found to be poorly differentiated, highly metastatic  
20 and did not require TSH for growth. The IR4 tumor was  
also obtained as a radiation induced rat thyroid  
carcinoma but IR4 is moderately differentiated into a  
follicular carcinoma, grows slowly only when TSH is  
provided and has low metastatic potential. IR6CL.sub.1 is  
25 a cell line derived from the IR6 tumor which retains the  
original properties of the parent IR6 tumor, e.g., it  
grows independently of TSH, is poorly differentiated and  
is highly metastatic.

30 An established epithelial cell line, FRTL5,  
derived from a culture of rat thyroid cells was also  
obtained. FRTL5 cells requires TSH and remains highly  
differentiated, but produces no tumors when injected  
subcutaneously into syngeneic Fischer 344 rats. Two

tumorigenic derivatives of the FRTL5 cell line, ELCL<sub>1</sub> and TRCL<sub>1</sub>, have also been isolated and characterized. ELCL<sub>1</sub> was obtained as a spontaneous mutant of FRTL5, and subsequently established as a transformed cell line which required low levels of TSH for growth. ELCL<sub>1</sub> formed primary tumors upon subcutaneous injection in syngenic rats but no metastasis was observed. TRCL<sub>1</sub> was a radiation induced mutant of FRTL<sub>5</sub> which was then established as a transformed cell line with no TSH requirement for growth. TRCL<sub>1</sub> cells produced fast-growing primary tumors with little or no potential for metastasis.

Some of the properties of the above described tumors and cell lines are summarized in Table 2.

TABLE 2  
Metastatic Potential of Rat  
Tumors and Rat Tumor Cell Lines

Tumors and Cell Lines	Spontaneous Metastases	Target Organs
Thyroid carcinoma		
IR6 tumor	high metastatic	Lung,
IR4 tumor	low metastatic	Liver,
		Kidney
Thyroid cell line		
FRTL5 (non-tumorigenic)	nonmetastatic	
ELCL <sub>1</sub> (tumorigenic)	nonmetastatic	
TRCL <sub>1</sub> (tumorigenic)	nonmetastatic	

#### EXAMPLE 4

##### Isolation of the Murine mts-1 Gene

5 mRNA from CSML-100 and CSML-0 cell lines was prepared as described by Chomczynski et al. supra, and polyadenylated mRNA was selected as in Sambrook et al. (Molecular Cloning: A Laboratory Manual, Vol. 1, Cold Spring Harbor Laboratory Press, 1989. Pages 7.1-7.29). 2  
10 µg poly (A)<sup>+</sup> mRNA from highly metastatic CMSL-100 cells was treated with reverse transcriptase under conditions appropriate to generate a single stranded complementary DNA (cDNA) (Sambrook et al., supra. Vol. 2. Pages 8.1-8.86). This CMSL-100 cDNA pool was subjected to  
15 subtractive hybridization with 50 µg poly (A) mRNA from low metastatic potential CMSL-0 cells to remove cDNA's with no role in the development of metastasis. The cDNA/RNA mixture was heated at 100°C for 5 min., cooled on ice and placed in a final reaction volume of 1 ml in  
20 7% phenol (adjusted to pH 7.6 with 0.1M Tris-HCl, 1.25M NaCl, 120 mM sodium phosphate buffer, pH6.8) in a 10 ml glass centrifuge tube in. The tube was shaken for 7 days at 25°C. After hybridization, the mixture was extracted twice with chloroform, dialyzed against 10 mM Tris-HCl  
25 (pH 7.5), 1 mM EDTA to remove excess salts, and then precipitated with ethanol. Double stranded cDNA/mRNA, representing functions which are not unique to the metastatic phenotype, were removed by passage through a hydroxyapatite column. The single stranded cDNA was made  
30 double stranded and cloned into a λgt10 vector by standard procedures (Sambrook et al., supra pages 8.1-8.86).



Functions expressed highly during metastasis were detected by differential hybridization with CSML-100 and CSML-0 P-labeled cDNA probes. Mouse mts-1 cDNA clones were identified as strongly hybridizing with the DCSM-100 probe but weakly hybridizing with the CSML-0 probe.

5

#### EXAMPLE 5

##### Isolation of a Rat mts-1 cDNA

5 Rat cDNA libraries were prepared from normal  
thyroid and radiation induced thyroid carcinoma tissues  
as well as cell lines derived from normal and  
carcinogenic thyroid tumor cells. Poly(A)<sup>+</sup> mRNA was  
purified from highly metastatic IR6 tumors and from low  
metastatic potential IR4 tumors. Single-stranded cDNA was  
10 synthesized from IR6 poly(A)<sup>+</sup> RNA and the IR6 mRNA was  
hydrolyzed. This IR6 cDNA pool was subjected to  
subtractive hybridization with a 50-fold excess of IR-4  
poly(A)<sup>+</sup> mRNA according to the phenol emulsion  
reassociation technique (PERT method) of Kohne et al.  
15 (1977, Biochemistry 16: 5329-5341). Single stranded cDNA,  
representing functions likely to be involved in the  
metastatic phenotype, was isolated from the subtractive  
hybridization mixture by passage through a hydroxyapatite  
column (which will bind double stranded nucleic acids,  
20 i.e. the RNA:DNA hybrids representing the IR6 functions  
of low metastatic potential) followed by alkaline  
hydrolysis of the remaining IR4 mRNA. The single-stranded  
cDNA pool was made double stranded and cloned into a  
λgt10 cloning vector.

25 The subtracted IR6 cDNA library was screened  
differentially with <sup>32</sup>P-labeled single stranded cDNA  
probes generated by treatment of IR6 and IR4 poly(A)<sup>+</sup>mRNA  
with reverse transcriptase. mts-1 clones were identified  
by strong hybridization with the IR6 probe but weak  
30 hybridization with the IR-4 probe.

## EXAMPLE 6

### Isolation of the Human mts-1 cDNA

5 A human cDNA library was constructed in  $\lambda$ gt10  
using poly (A) <sup>+</sup> RNA prepared from HeLa cells. The  
library was screened with a <sup>32</sup>P-labelled mouse mts-1 cDNA  
probe at 420 in 50% formamide. Filters were washed in 2 x  
10 0.2 x SSC with 0.1% SDS at room temperature and then twice in  
0.2 x SSC with 0.1% SDS at 50°C. Strongly hybridizing  
cDNA clones were sequenced; the human mts-1 cDNA was  
identified by high sequence similarity to the mouse mts-1  
cDNA in regions outside the highly conserved Ca<sup>++</sup> binding  
domain. This human mts-1 clone is full length as judged  
15 by sequencing of the human genomic mts-1 gene and by  
primer extension analysis of mts-1 mRNA using mts-1  
oligonucleotide probes. The nucleotide and amino acid  
sequences of the human mts-1 gene are provided as SEQ ID  
NO: 1 and 2, and also given in FIGS. 1 and 2.

20 The mts-1 cDNA was also isolated from human  
melanoma cell line Wm64 by reverse transcription of mRNA  
isolated from those cells followed by polymerase chain  
reaction.

### Reverse Transcriptase Polymerase Chain Reaction (RT-PCR)

25 Total RNA from human melanoma cell line Wm64  
was pretreated with RNase free DNase I (1U/ $\mu$ l) in 2 mM  
MgCl<sub>2</sub> for 30 minutes at 37°C then 95°C for 5 minutes to  
inactivate the DNase; poly A<sup>+</sup> RNA was not routinely  
30 treated with DNase I before an RT-PCR experiment. RNA (1  
 $\mu$ g total RNA or 50 ng poly A<sup>+</sup> RNA) was reverse  
transcribed in the presence of 50 mM Tris-HCl pH 8.3, 75

mm KCl, 3 mM MgCl<sub>2</sub>, 3 μM oligo-dT<sub>15</sub>, 0.3 mM each dNTP, 200 U M-MLV reverse transcriptase at 22°C for 10 minutes, 42°C for one hour and 90°C for 10 minutes. The following human mts-1 primers were used for synthesis of the human mts-1 cDNA by PCR reaction:

5' ATG GCG TGC CCT CTG GAG AAG - 3' (SEQ ID NO:8)

5' TTT CTT CCT GGG CTG CTT ATG - 3' (SEQ ID NO:9).

PCR amplification was done in 10 mM Tris HCl (pH 8.4), 50 mM KCl, 1.5 mM MgCl<sub>2</sub>, 0.01% gelatin with 2.5 mM dNTP, 0.6 μM each primer and 1.25 U Taq DNA polymerase.

Amplification was by 35 cycles of: 94°C for 1 min; 52°C for 2 min; 72°C for 3 min, followed by a 7 min extension period at 72°C.

Amplified DNA was isolated from a 1% agarose gel and cloned into a baculovirus transfer vector as described in Example 7.

#### EXAMPLE 7

##### Expression of the mts-1 Gene Product

Overexpression of the mts gene product, is  
5 accomplished by DNA transfections using the vector system  
described by Lockshon and Weintraub. This vector is a  
pUC19 based vector system, very similar to the  
Bluescript.TM. vector (FIG. 3). In the unique HindII site  
10 of the Bluescript.TM. vector, a eukaryotic control  
element harboring a strong murine sarcoma virus promoter,  
followed by a unique EcoRI site, followed by SV40  
polyadenylation sequences is introduced. The complete  
mts-1 cDNA is introduced into the unique EcoRI site  
15 downstream from the MSV-LTR sequences. Because of the  
presence of an internal EcoRI site in the mts-1 cDNA,  
partial EcoRI digestion of the mts-1 recombinant is done  
to isolate the entire mts-1 cDNA molecule. Retroviral  
promoters with LTRs are very strong and overexpression of  
the mts transcript is expected. The mts-1 recombinant  
20 expression vector can be used for both permanent or  
transient expression. However, stable (permanent)  
transfectants are desirable because stable transfectants  
can be clonally purified, and represent a homogeneous  
population of a given phenotype useful for quantitating  
25 metastatic potential.

##### Expression of mts-1 protein from a pTrcHisB vector:

Large quantities of the mts-1 specific protein  
were expressed using the inducible bacterial vector  
30 pTrcHisB (Invitrogen) (FIG. 10a). Murine mts-1 cDNA was  
subcloned in frame (confirmed by sequence analysis) into  
a BamHI-KpnI site with the multiple cloning site of

pTrcHisB. This generated plasmid pTBM1. The fusion protein expressed by pTBM1 had 6 tandem histidine residues (which have a high affinity for a  $\text{Ni}^{++}$  charged resin), an enterokinase specific cleavage site, and the mts-1 protein product. Expression of the fusion protein encoded by pTBM1 was induced by IPTG. Similar constructs were generated with human mts-1 cDNA.

Expression of mts-1 protein in a baculovirus expression vector:

A plasmid containing the cytomegalovirus promotor was used to construct pCMV/mts-1<sub>h</sub> or pCMV/mts-1<sub>m</sub> high expression vectors harboring mts-1 human and murine cDNAs, respectively.

The baculovirus expression vector mts-1-BacPAK<sub>6</sub> plasmid was constructed from the pCMV clones as follows. pCMV-mts-1 was digested with BamH1, and the mts-1 cDNA fragment was purified from a 1% agarose gel. The purified fragment was ligated into BamH1-cleaved pBacPAK1 and the ligation mix was transformed into E. coli JM109 cells. Positive clones were identified and plasmid DNA was sequenced to confirm the orientation and integrity of the ligation junction.

Transfer vector pBacPAK-mts-1 was transfected into Sf21 cells, along with Bsu361 digested BacPAK6 viral DNA. Soon after infection, the cells were overlaid with 1% agarose to visualize the plaques and to prevent mixing of clones. After 4-5 days of infection, the cells were stained with neutral red which is taken up by healthy cells, but not by the dead cells. Plaques appeared as clear circles against red or pink background.

Western Blot analysis using the  $\alpha$ -mts-1 antibody was conducted to confirm that several mts-1 recombinant viruses produced mts-1 proteins.

## EXAMPLE 8

### Purification of mts-1 Protein

5                   Purification of the mts-1 protein parallels  
that of other S100 family members which have been  
purified to homogeneity from bovine brain (Baudler, et  
al. J. Biol. Chem. 261: 8204-8212, 1986). Exceedingly  
10 high degrees of purification can be achieved because of  
the stability of the protein and the availability of  
several affinity chromatography steps including  
phenothiazine-agarose, zinc dependent binding to phenyl  
sepharose. FPLC chromatography on Mono Q is known to  
15 separate S100 family members and other HPLC columns have  
been developed such as melittin silica, to affinity  
purify S100 proteins. Tissues or cells providing large  
amounts of mts-1 include not only the bacterial, yeast  
and mammalian cell lines engineered to express large  
20 quantities of recombinant mts-1, but also the highly  
metastatic tumors and cell lines shown to express mts-1  
by the present  
invention.

### Purification of His-mts-1 Fusion

25                   An overnight culture transformed with pTBM1 was  
diluted 1:100 and allowed to grow 1.5 hours  
(until  $OD_{600} = 0.3$ ). The culture was then induced with 1 mM  
1PTG and allowed to grow 4.5 hours more at 37°C. Cells  
30 were harvested, cell pellets were then collected by  
centrifugation and resuspended in a 6M guanidinium-HCl  
buffer. The cells were stirred for 1 hour and then



centrifuged at 18K rpm for 15 min at 4°C. The supernatant was collected and added to a 50% slurry of Ni<sup>++</sup> NTA resin (obtained from Qiagen). The mixture was stirred for an hour and loaded onto a column. The column was washed in a series of urea based buffers which differed only in pH (each wash being of a lower pH). The protein was eluted in 3 ml fractions using buffer D (8M urea, 0.1M Na Phosphate, 0.01M Tris/HCl, pH 5.9). A large amount of the protein did not elute until the pH of the buffer was lowered to 4.5 (buffer E): monomeric forms of the histidine fusion eluted in buffer D, whereas aggregates eluted in buffer E. Aliquots of each fraction were boiled in SDS-PAGE loading buffer and loaded onto 12% SDS-polyacrylamide gels. The gels were stained with Coomassie Brilliant Blue. The results of such experiments are depicted in FIG. 10b. After the purity of the His-Mts1 fusion protein was confirmed, assays were performed to determine relative protein concentrations. Fractions D2 and E1 (which contained approximately 3.2 mgs protein total) were pooled and run on another SDS-polyacrylamide gel. Strips were cut out from the gel and stained in Coomassie Brilliant Blue to determine the location of the His-Mts1 protein in the gel. The portion of the gel containing the His-Mts1 fusion was cut out and the protein was isolated from the gel by elution.

## EXAMPLE 9

### Generation of Polyclonal Antibodies

#### Antibodies Against mts-1 Peptides

Synthetic oligopeptides with the following amino acid sequences were made:

1) Human mts-1 amino acids 2-11 (unique):

Ala-Cys-Pro-Leu-Glu-Lys-Ala-Leu-Asp-Val

2) Human mts-1 amino acids 22-37 (the calcium binding domain):

Lys-Glu-Gly-Asp-Lys-Phe-Lys-Leu-Asn-Lys-Ser-Glu-Leu-Lys  
Glu-Leu

3) Human mts-1 amino acids 42-54 (unique):

Leu-Pro-Ser-Phe-Leu-Gly-Lys-Arg-Thr-Asp-Glu-Ala-Ala

4) Human mts-1 amino acids 87-101 (unique):

Asn-Glu-Phe-Phe-Glu-Gly-Phe-Pro-Asp-Lys-Gln-Pro-Arg-  
Lys-Lys

Peptides 1, 3 and 4 were chosen as mts-1 antigens because they encode unique proteins of the mts-1 protein, i.e. these regions of the mts-1 protein do not share homology with other proteins, in particular with other calcium binding proteins. Peptide 2 was chosen because it encodes the calcium binding domain of mts-1. Therefore, peptide 2 generates antibodies reactive with many members of the calcium binding protein family.

New Zealand white female rabbits were immunized by subdermal injection with 100  $\mu$ l of Freund's complete adjuvant containing 0.1-1 mg of oligopeptide in 10 locations along the back. The rabbits were first shaved on both sides of the back for easy subdermal injection. The antigen-adjuvant mixture was prepared by mixing in

two connected 1 ml glass teflon syringes. Typically rabbits are then injected with about 1 mg of antigen at each 2 month interval following the primary injection, until the serum is positive at a dilution of greater than  $10^{-4}$  when assayed by immunoblotting.

#### Antibodies Against Whole mts-1 Protein

The mts-1 protein was expressed as a His-Mts1 protein (Examples 7 and 8). Host cell lysates containing the His-Mts1 protein were fractionated over a  $\text{Ni}^{++}$  NTA column (Qiagen). Fractions containing the most His-Mts1 protein were pooled and electrophoresed on an SDS-polyacrylamide gel. The purified protein was eluted from the gel and sequenced to confirm that it was His-Mts1.

Three chickens were then immunized with the purified His-Mts1 protein. Chickens were chosen for two reasons. First, mts-1 is highly conserved in mammals and an avian system was expected to provide a better immune response. Second, antibodies can easily be obtained from the eggs of the chickens. Continuous bleeding of the animal to obtain antibodies is, therefore, avoided.

The polyclonal antibody generated was named  $\alpha$ -mts-1, and its efficacy on Western blots and tissues was established (see Example 16 and FIGS. 13 and 14).

#### EXAMPLE 10

##### Monoclonal Antibody Production

Monoclonal antibodies are prepared in accordance with the techniques developed by Kohler and  
Mulskin (Eur. J. Immunol. 6:511-519, 1976) and Harlow et  
al. (Antibodies: A Laboratory Manual, Cold Spring Harbor  
Laboratory Press, 1988). Balb/c mice are immunized  
subdermally with 100 µl of Freund's complete adjuvant  
containing 0.1-1 mg of the conjugated or non-conjugated  
mts-1 oligopeptides described in Example 9. Two weeks  
after the initial injection, the mice are boosted  
with the appropriate mts-1 antigen by intravenous and  
intraperitoneal injection of 100 µg of antigen in  
phosphate buffered saline (PBS).

Five days after the last injection and after  
confirmation of the presence of antibody in mouse sera,  
the mice are sacrificed and their spleens removed. Spleen  
cells are obtained by gentle disruption of the spleen in  
a 7 ml Dounce homogenizer in 3.5-4 ml PBS. The cells are  
then pelleted at 1200 rpm in a PR6 centrifuge for 6  
minutes at room temperature. The supernatant is removed  
into a suction flask, and the cells are resuspended in 15  
ml 0.83% NH<sub>4</sub> Cl. This suspension is incubated at room  
temperature for 5 minutes then underlain with 10 ml fetal  
calf serum at 37° C. The cells are again pelleted by  
centrifugation for 8 minutes, at 1200 rpm at room  
temperature, then the supernatant is withdrawn into a  
suction flask cells resuspended in 20 ml PBS.

The following solutions are prepared for use in  
the subsequent cell fusion:

Hypoxanthine (H), 680 mg/100 ml H<sub>2</sub>O; add 204 drops conc. H<sub>2</sub>SO<sub>4</sub>; heat to dissolve Aminopterin (A), 46.4 mg/100 ml H<sub>2</sub>O; add 2 drops 1.0N NaOH to dissolve Thymidine (T), 775 mg/100 ml H<sub>2</sub>O; add 45 mg glycine;

5 PEG-DME--melt PEG at 42°C., then add 1 ml DME (at 37°C.); adjust pH with 1.0N NaOH to 7.6;

DMEM--to 500 ml DME add 37.5 ml a- horse serum; 37.5 ml FCS, 10.0 ml L-glutamine, 0.2 ml garamycin;

10 2X HAT-DME--to 200 ml DME add 25.0 ml a- horse serum, 25.0 ml FCS, 4.0 ml L-glutamine, 0.2 ml garamycin, 0.8 ml H, and 0.8 ml A, and 0.8 ml T (2X HT-DME omits A);

Cloning Agar--350 mg unwashed Difco agar in 25 ml H<sub>2</sub>O, autoclaved;

15 Cloning Medium--to 25 ml 2X DME, add 35 ml filtered, condition DMEM, 7 ml a- horse serum, 7 ml FCS, 1 ml L-glutamine, 0.1 ml garamycin.

20 Two 30 ml flasks of plasmacytoma P3 NS1/1-Ag4-1 cells are added to centrifuge tubes and spun down at 1200 rpm for 8 minutes at room temperature. The spleen cells are resuspended in 20 ml PBS. From each suspension, 0.01 ml is removed and added to 0.1 ml 0.4% trypan blue and 0.3 ml PBS and the cells counted. The volume of each suspension is adjusted so as to obtain a spleen cell to NS1/1-Ag4-1 cell ratio of 10:1, and the suspensions are  
25 then mixed. The mixture is pelleted at 1200 rpm for 8 minutes at room temperature and all but about 0.1 ml of supernatant removed. The cells are then resuspended in the remaining liquid and then added to 1.3 ml of 1:1 PEG-DME solution, pH 7.6. Every minute the volume of the  
30 solution is doubled with DME until the final volume is 25 ml.

The cells are again pelleted, the supernatant decanted, and the cells resuspended in enough 50% 2X HAT-DME/50% conditioned DMEM (the supernatant retained from the Sp2/0 cells above) to yield a final concentration of about  $3.5 \times 10^6$  spleen cells. The cells are distributed into a 96-well flat-bottom microtiter plate (TC-96; Flow Laboratories), at 0.1 ml/well. The plate is incubated at 37°C in humidified air/CO<sub>2</sub> until visible colonies appear, usually about 10-12 days. The contents of the well is transferred to 0.5 ml of HAT-DME/conditioned DME in a TC-24 plate (Flow Laboratories). When healthy cell growth appears (about 2-5 days), about 0.35 ml medium is removed and tested for antibody production by enzyme-linked immunosorbent assay (ELISA), hemagglutinin inhibition assay, or neuraminidase inhibition assay. When those cells producing the antibodies of interest are growing well, one drop for each culture is transferred into 1.0 ml DMEM in a TC-24.

To clone the hybrid cells, 25 ml of melted agar and 76 ml of cloning medium is combined, and 5 ml is pipetted into 60 mm petri dish and left to solidify. Cells from DMEM cultures are diluted in 50% DMEM/50% conditioned DMEM,  $10^{-1}$  or  $10^{-2}$  depending on cell growth. Into sterile tubes is placed 0.1 ml of each of the two dilutions, and to each is added 0.9 ml of cloning medium/agar mixture. This is mixed well and poured over the surface of the agar underlay. After solidification the plates are incubated at 37°C incubator until colonies are visible with the naked eye, typically about 7-10 days. Colonies are then picked and transferred 0.1 ml of DMEM/conditioned DMEM in a TC-99 plate and incubated at

37°C in a CO<sub>2</sub> incubator. After the culture is acidic (usually 1-4 days), transfer is made to 0.05 ml DMEM in TC-24 plate. When the growth is 50% confluent, the medium is removed and tested for antibody production are previously. Those clones producing mts-1 specific antibodies are moved into 5 ml DMEM in 25 cm<sup>2</sup> flasks. Cloned cells are then frozen or injected into mice for ascites production.

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#### EXAMPLE 11.

##### Sandwich Assay For mts-1

For detection of the presence of mts-1 in serum or cleared cell lysates of tissue specimens, approximately 100 ul of a monoclonal antibody prepared as in Example 9 or 10 is immobilized on latex beads and is contacted with about 100 ul of the serum or cleared lysate to be tested. The immobilized antibody and lysate are allowed to react for a period of about ten minutes and then the latex beads with the mts-1 antigen bound to the immobilized antibody are rinsed with a solution of PBS (phosphate buffered saline). To the latex beads is then added about 100 ul of mts-1 specific antibody conjugated to horseradish peroxidase. The labeled antibody bead mixture is incubated for a period of about ten minutes. At this time, an enzyme substrate, hydrogen peroxide and aminoantipyrine, are contacted with the beads, and this mixture is incubated for a period of about 5-10 minutes, at which time the development of color in the sample is an indication of a positive reaction and the presence of mts-1.



#### EXAMPLE 12

##### Expression of mts-1 is 10-100 Fold Higher in Metastatic Tumor Cells Than in Non-Metastatic Cells

To examine the expression levels of mts-1, mRNA was purified from metastatic and benign tumors, and cell lines derived from such tumors, as well as from corresponding normal tissues. Purified RNA was size fractionated in a gel and blotted onto nylon membranes for Northern analysis with mts-1 nucleic acid probes.

FIG. 4 shows that the CSML-0 cell line of the present invention, which has a very low metastatic potential, had very low, or non-detectable levels of the mouse mts-1 transcript. In contrast, the CSML-100 cell line of the present invention, which has an extremely high metastatic potential, expressed high levels of mts-1. It is estimated that metastatic CSML-100 cells express at least 100-fold more mts-1 than do non-metastatic CSML-0 cells.

Similarly, in a separate experiment, various metastatic and non-metastatic tumors and tumor cell lines were tested for their mts-1 expression levels, by Northern analysis using a <sup>32</sup>P-labeled mouse mts-1 probe. The properties of these tumors and cell lines are described in detail in Examples 1, 2 and 3 and in Tables 1 and 2. As shown in FIG. 5, only those tumors and cell lines which are metastatic (indicated by an "M" above the gel lane) exhibit high levels of mts-1 expression. Metastatic cell types exhibiting increased mts-1 expression include: RL-67 lung carcinoma tumors, Lewis Lung carcinoma tumors, LMEC embryo-carcinoma tumors, and T-36 embryo-carcinoma tumors and cell lines.

FIG. 6 shows that the highly metastatic adenocarcinoma rat tumor, IR6 (lane 5), and a cell line derived from IR6 (lane 7), as well as a metastatic cell line derived from a mouse lung carcinoma, Line 1 (lane 3) all exhibit 10-100 fold increased levels of mts-1 expression compared to a tumorigenic but non-metastatic cell line, TRCL<sub>1</sub> (lane 6) or a non-tumorigenic FRTL5 cell line (lane 8).

Hence these data demonstrate unequivocally that mts-1 expression is increased 10-100 fold in metastatic cells of diverse types relative to normal cells or non-metastatic (benign) tumor cells.

Table 3 further illustrates that only metastatic cells or cells with a high degree of motility express high levels of mts-1 RNA. Detection was by northern analysis using  $\gamma$ -actin expression for normalization. Autoradiograms were densitometrically traced, and a numerical value between 0-5 was assigned relating the tracing peak height to the amount of expression. The status of each cell type tested was characterized as normal (N), benign (B), metastatic (M) or cell line (C). The number of samples tested is indicated under the status of cell type.

Table 3 illustrates that only metastatic cell types have an mts-1 expression level greater than 0.5. Accordingly, high levels of mts-1 expression are observed in numerous metastatic cell types including, for example, liver hepatomas, lung carcinomas, pancreatic cancers, breast adenocarcinomas, endometrial cancers, ovarian cancers, cervical cancers, melanomas, lymphomas and leukemias. However, such high levels of mts-1 expression are observed only in metastatic cells,

non-metastatic cells do not express high levels of mts-1.

TABLE 3

Selective Expression of mts-1 in Metastatic  
Cells or Cells with High Degree of Motility

	Phenotype of Tissue	No. of Samples; Status				Level of Expn.
		N	B	M	C	
10	Adult Liver	5	-	-	-	0
	Liver Adenoma	-	5	-	-	0
	Liver Hepatoblastoma	-	5	-	-	0
	Liver Hepatoma	-	-	4	-	1.0
	Adult Colon	4	-	-	-	0.4
15	Colon Carcinoma	-	5	-	-	0.43
	Adult Kidney	2	-	-	-	0.1
	Kidney Carcinoma	-	2	-	-	0.1
	Adult Lung	2	-	-	-	0.1
	Small Lung Carcinoma	-	-	2	-	1.0
20	Adult Pancreas	1	-	-	-	0
	Pancreatic Cancer	-	-	1	-	1.0
	Normal Breast	4	-	-	-	0
	Breast Carcinoma	-	2	-	-	0
	Breast Adenosarcoma	-	-	-	2	1.0
25	Endometrial Cancer	-	-	2	-	1.5
	Ovarian Cancer	-	-	2	-	1.4
	Cervical Cancer	-	-	2	-	1.5
	ASPC 1 Pancreatic Cancer	-	-	-	1M	1.0
	AN3CA Endometrial Cancer	-	-	-	1M	1.5
30	BIX3A Ovarian Cancer	-	-	-	1M	1.5
	Hela Cervical Cancer	-	-	-	1M	1.5
	MCF7-1 Breast Cancer	-	-	-	1	0
	AS49-1 Lung Cancer	-	-	-	1 (M)	0.8
	MC1 Neuroblastoma Line	-	-	-	1	0
35	Y79 Retinoblastoma	-	-	-	-	0
	Primary Melanoma Wm278	-	-	-	1	0.5
	Corcl Primary Melanoma	-	-	-	0	1.0
	Wm8 Melanoma	-	-	-	1 (M)	2.0
	Wm164 Melanoma	-	-	-	1 (M)	2.0

Normal B Cells Do Not Express mts-1

B-Cell Lymphoma & Leukemias

	Type	No.	Level of Expn.
45	Cleaved B Cell Lymphoma	1	3
	Hairy Cell Leukemia	1	4
50	CML Crisis B Cells	3	3

TABLE 3 (CONT.)

5	<u>Leukemias</u>	No. of Samples <u>Tested</u>	Average <u>mts-1</u> Expn. <u>Level</u>
	<u>Type</u>		
10	CML (chronic probe)	23	0.49
	CML (crisis)	12	1.9
	CMML	1	1.0
	ALL	1	3.0
	AML	6	0.7
	AMML	2	1.0
15	Pure Monocytic Leukemia	3	1.5
<u>Abnormal Blood Infiltrated with High WBC</u>			
<u>Count Separated by Ficoll-Hypaque Gradient</u>			
20	Pellet	4	0.3
	Interface	5	0.6

25

### EXAMPLE 13

#### Introduction of the mts-1 Gene into Cultured Cells Confers a Metastatic Phenotype

5           According to the present invention, mts-1 is  
not expressed in normal, or nonmetastatic tumor cell  
lines, from the rat thyroid or the mouse lung. However,  
the highly metastatic Line 1 cell line, derived from a  
10 mouse lung carcinoma, does express mts-1 mRNA. When Line  
1 cells are grown in the presence of 3% DMSO, they lose  
their metastatic potential and also do not show  
detectable levels of mts-1 mRNA. These data indicated  
that mts-1 expression is correlated with the metastatic  
15 phenotype.

To establish that high levels of mts-1  
expression can confer a metastatic phenotype the rat  
mts-1 cDNA was cloned into the MSV vector depicted in  
FIG. 3, to allow high expression of the mts-1 protein.  
20 This mts-1 expression vector was co-transfected into  
mouse lung carcinoma Line 1 cells with a plasmid encoding  
a selectable neomycin (Neo) gene. Stable cell lines  
resistant to neomycin were tested for integration of the  
mts-1 gene into their genome by Southern blot analysis of  
25 their genomic DNA. The controls for this experiment were  
Line 1 cells stably transfected only with the selective  
neomycin resistance gene grown in the presence of 3%  
DMSO, as well as non-transfected Line 1 cells grown  
without DMSO.

30           Ten transfectants (N1-N10) possessing the  
transfected mts-1 gene were grown in 3% DMSO to test  
whether acquisition of the highly expressed recombinant  
mts-1 gene could generate a metastatic phenotype in cells  
that are normally not metastatic.  $10^5$  cells of

transfectants N2, N3, N4, N5, and N8 were injected in the tail veins of 3 mice. As controls,  $10^5$  cells of Line 1 cells, and two neomycin only transfectant cell lines (Neo 2 and Neo 3) were injected into the tail veins of 3 mice. The animals were sacrificed after 2 weeks and tested for lung metastasis after staining with India ink and fixation. The animals injected with N4 and N5 cells grown in 3% DMSO prior to injection, exhibited high levels of metastasis, equivalent to Line 1 cells grown in the absence of DMSO, while other cell lines gave rise to low levels of metastasis. The fact that not all transfected cell lines gave rise to high levels of metastasis might have been due to a variation in mts-1 expression levels caused by mts-1 insertion into "silent" regions of the genome. To examine the expression levels of mts-1 in N1-N10 transfectants grown in 3% DMSO, mRNA was extracted from these cell lines prior to injection into mice, and analyzed for mts-1 mRNA expression levels by Northern analysis. As shown in FIG. 8, not all transfectants exhibit high levels of mts-1 expression, probably because of the influence of genomic regulatory elements lying near the mts-1 insertion site. Transfectant cell lines N3, N4 and N5 have high levels of mts-1 expression, but the N3 cell line gives rise to a low molecular weight mts-1 transcript, indicating that the mts-1 gene of this transfectant cell line may be defective due to a rearrangement during transfection and integration into the genome.

Table 4 shows that similar data were obtained by intravenous injection into rats of transfectant cell

lines containing expression vectors with the rat mts-1 gene in a sense and antisense orientation, relative to the MSV LTR promoter.

5           Hence, these data indicate that the metastatic phenotype can be generated in non-metastatic cells by the introduction of a highly expressed mts-1 gene.



TABLE 4  
Mouse Lung Metastasis Counts  
Using Different mts-1 Transfectants

	Neo+	Line I+		Clone 156/3 (N <sub>3</sub> )+	Clone 156/4 (N <sub>4</sub> )+	Clone 156/5 (N <sub>5</sub> )+
	DMSO	DMSO	Line I	DMSO	DMSO	DMSO
Intravenous		5	57	190	342	355
Injection		0	38	205	300	495
10 <sup>5</sup> Cells		0	65	251	320	310
Into Tail		11	68	300	75	142
Vein						120

rat mts1 clone 156 = sense construct

rat mts1 clone 162 = antisense construct

In the above experiment IR6 tumor cells alone generate lung metastasis in 20% of the injected rats, with 1-2 tumors observed in the kidneys of some rats. 50% of rats injected with transfectants containing mts-1 in a sense orientation (cell lines 156/2, 156/7 and 156/8) had metastases, while 10% of rats injected with transfectants containing mts-1 in an antisense orientation (cell lines 162/9 and 162/1) had metastases.

Hence transfection of a mammalian mts-1 gene into mice or rat cells can cause such cells to undergo metastasis when they are injected into a mouse or rat.

#### EXAMPLE 14

##### CSML-100 Cells Grow More Slowly than CSML-0 Cells

###### Methods:

CSML-0 and CSML-100 cells were seeded at a density of  $10^6$  cells/dish and counted the following day using a hemacytometer. The relative rates of DNA synthesis were measured by incorporation of  $^3\text{[H]}$  thymidine. Both experiments were done in triplicate, and the data are reported as an average.

DNA synthesis was measured as follows. The cells were washed once with media. 2 mls of media containing 1  $\mu\text{l}$  of  $^3\text{[H]}$  thymidine was added to the cells and incubated for 4 hours. The cells were washed twice with PBS and TCA precipitated following standard protocols. The TCA precipitate was dissolved in 0.1N NaOH containing 0.5% Triton X-100 and placed on ice for 30 minutes. The resultant suspension was added to 6 mls of scintillation fluid for scintillation counting.

###### Results:

Table 5 illustrates that less cell growth and less tritiated thymidine incorporation was observed for metastatic CSML-100 cells than for non-metastatic CSML-0 cells.

TABLE 5

Cell Line	$^3\text{[H]}$ Thymidine Incorporation (dpm)	Cells/Dish	DNA Synthesis/Cell
CSML-0	6428	$1.6 \times 10^6$	$4.0 \times 10^{-3}$
CSML-100	3700	$1.1 \times 10^6$	$3.3 \times 10^{-3}$

In particular, only  $1.1 \times 10^6$  CSML-100 cells are observed per dish, whereas  $1.6 \times 10^6$  CSML-0 cells are observed.

5 Since  $1 \times 10^6$  cells of both type were plated, the CSML-100 cell growth was only about one-sixth that of the CSML-0 cell growth. FIG. 11 further illustrates that the growth of CSML-100 cells from a 2-day to at least a 5-day period is less than that of CSML-0 cells.

10

# BOOK REVIEW

#### EXAMPLE 15

### mts-1 mRNA Can Be Detected by Hybridization of mts-1 Antisense Probes to Tissue Sections

#### Methods

Mouse embryonic trophoblast cells express mts-1. To illustrate the efficacy of mts-1 nucleic acid probes for detection of mts-1 mRNA in tissue sections, frozen sections of an 8 day mouse embryo were obtained. Sections were placed onto a standard microscope slide and fixed for 5 min. with 3% formaldehyde, 0.1M phosphate buffer, pH 7.2.

Sense and antisense mts-1 riboprobes were prepared by in vitro transcription from a GEM-2-mts-1 vector containing the 3'untranslated region of mts-1 using T<sub>7</sub> and T<sub>3</sub> RNA polymerases according to the manufacturers direction. Transcription was with <sup>3</sup>H-UTP (45 µG, Amersham).

Prior to hybridization, slides were acetylated with 0.25% (v/v) acetic anhydride in 0.1M triethanolamine for 10 minutes at room temperature. The sections were rinsed in 2X SSC and dehydrated through an ethanol series (30%, 50%, 70%, 85%, 95%, 99%, 99%).

To the dried sections, 20 µl of hybridization solution (0.3M NaCl, 20 mM Tris pH 8, 1 mM EDTA, 50% formamide, 10% dextran sulfate, 1X Denhardt's, 500 µg/ml yeast RNA) containing about 10<sup>4</sup> cpm/µl <sup>3</sup>H sense or antisense probe, preheated to 80°C, was applied and secured with a coverslip. The slides were immersed in mineral oil and incubated at 45°C for about 12 hours. Excess mineral oil was removed from slides, and slides were washed through chloroform 3 times. Slides were next

5 rinsed 3.times.5 in 4X SSC to remove coverslips. RNase digestion (20 µg/ml RNase A, 1 U/ml RNase T<sub>1</sub>) in 0.5M NaCl, 10 mM Tris pH 8.0, 1 mM EDTA) was done for 30 minutes at 37°C. Slides were washed once in RNase buffer for 30 minutes, 37°C; then in 4 liters 2X SSC for 30 minutes at room temperature; next in 0.1X SSC at 55°C for 30 minutes; finally in 4 liters 0.1X SSC at room temperature for 30 minutes. Slides were dehydrated through an ethanol series containing 300 mM ammonium acetate. Once slides were dry, they were dipped in NTB-2 emulsion (Kodak) diluted 1:1 with 600 mM ammonium acetate and autoradiographed for 4 weeks. Slides were developed in D-19 2.5 minutes, fixed in 2% acetic acid 30 seconds, fixed for 5 minutes and rinsed in water for 30 minutes. Finally, sections were counter stained, cover slipped and photographed using dark-field illumination.

### Results

20 Hybridized mts-1 probe was detected in mouse trophoblast cells only when the mts-1 probe was an antisense probe (FIG. 12a). The sense mts-1 probe gave rise to no signal (FIG. 12b). These data indicate that an antisense mts-1 probe can be used to detect mts-1 mRNA in tissue sections.

## EXAMPLE 16

### Chicken Anti-mts-1 Antibody Detects mts-1 Protein by Western Blot and Immunohistochemistry

#### Methods:

The chicken anti-mts-1 antibody ( $\alpha$ -mts-1) was prepared as described in Example 9.

Lysates of CSML-0 and CSML-100 cells were electrophoresed on 12% SDS-PAGE gels and transferred to polyvinylidene difluoride (PVDF) membranes for Western blot analysis. Membranes containing 3  $\mu$ g purified mts-1 were incubated with anti-mts-1 antibody (1:2000) for 3 hours at room temperature and then with anti-chicken IgG-HRP at room temperature for 2 hours. Signal was detected with diaminobenzene (DAB).

To test the specificity of the  $\alpha$ -mts-1 antibody, membranes containing CSML-100 proteins were probed with  $\alpha$ -mts-1 in the presence and absence of 260 ng free recombinant mts-1 protein. Membranes containing 3  $\mu$ g purified mts-1 were treated as above but upon addition of the primary antibody ( $\alpha$ -mts-1) 13  $\mu$ g of purified free mts-1 was added.

Frozen mouse spleens were sectioned and fixed onto glass slides. Sections were probed with a 1:1000 dilution of  $\alpha$ -mts-1 in PBA according to the method of Harlow et al. To test the specificity of the  $\alpha$ -mts-1 antibody, 130 ng free mts-1 protein was applied to one series of slides along with the diluted  $\alpha$ -mts-1 antibody.

The  $\alpha$ -mts-1 antibody was deemed specific for mts-1 protein when free mts-1 effectively eliminated binding of  $\alpha$ -mts-1 to mts-1 Western blots or mouse spleen sections.

Results:

FIG. 13 depicts a Western blot of CSML-0 (Lane 1) and CSML-100 (Lanes 2 and 3) cell lysates. Lanes 1 and 2 were probed with  $\alpha$ -mts-1 antibody without added free mts-1 protein. As illustrated, a 10-12 Kd mts-1 protein is expressed in CSML-100 cells (Lane 2) but not in CSML-0 cells (Lane 1). Moreover, 260 ng free mts-1 protein effectively eliminated antibody binding to the CSML-100 cell lysate in Lane 3. Therefore, the  $\alpha$ -mts-1 antibody is highly specific for mts-1 protein.

Similarly, mts-1 protein is detected in frozen mouse spleen sections (FIG. 14a) and  $\alpha$ -mts-1 antibody binding on such tissue sections is eliminated when free mts-1 protein is applied to the sections with the antibody (FIG. 14b).

Accordingly, mts-1 protein can readily be detected on Western blots and on tissue sections using the  $\alpha$ -mts-1 antibody.

### EXAMPLE 17

#### Low Molecular Weight mts-1 Protein is Found Only in Serum From Animals with Metastatic Cancer

##### Methods:

Mouse Studies: CSML-0 and CSML-100 cells were injected intravenously into the tail veins of A/J mice at  $1 \times 10^5$  cells per mouse (FIG. 15a, Lane 2) or  $1 \times 10^6$  cells per mouse (FIG. 15b, Lane 2). After three weeks the mice were sacrificed, their lungs examined for the presence of metastasis, and their blood drawn. Blood was allowed to clot at room temperature for one hour and was then microfuged to isolate sera. The sera samples were loaded at 100  $\mu$ g per lane on a 13% SDS-PAGE gel (FIG. 15a) or a 13% Tris-Tricine gel (FIG. 15b). The proteins were then transferred to PVDF membranes and probed with a 1:1000 dilution of  $\alpha$ -mts-1 antibody and a horse-radish peroxidase conjugated secondary antibody.

mts-1 is expressed in T lymphocytes and activated macrophages. To test whether the detected mts-1 protein resulted from lysis of normal blood cells including T lymphocytes and macrophages, whole mouse blood was lysed and probed with  $\alpha$ -mts-1 antibody in a western blot analysis.

Whole blood was taken from a normal mouse, lysed in a triton-X100 solution and electrophoresed on a 13% Tris-Tricine gel. A PVDF membrane blot of the gel was prepared and probed as above.

To determine whether the presence of mts-1 in sera is simply due to a chronic immune response



which might increase the number of T lymphocytes and activated macrophages, mice were injected with salmonella LPS over an extended time period to induce a chronic immune response. Sera were drawn and western analysis was performed as described above.

Human Studies: Serum samples were obtained from normal women and patients with breast carcinomas or advanced malignant lymphomas 150 µg of each serum sample was run on a 12% SDS-PAGE gel. The proteins were transferred to PVDF membranes and the membranes were probed with a 1:1000 dilution of  $\alpha$ -mts-1 and then with a 1:1000 dilution of the secondary antibody (rabbit anti-chicken IgG-HRP). The reaction was developed with a DAB solution.

#### Results:

Mouse Studies: Three weeks after intravenous injection, the mice receiving CSML-100 looked very sick and had breathing difficulties. Western analysis of sera from injected and non-injected animals indicated that only those mice receiving CSML-100 cells had a 10-12 Kd mts-1 protein (FIGS. 15a and 15b, Lane 2). Injection of as little as  $10^5$  CSML-100 cells three weeks prior to western analysis produced a positive serum response. The lungs of those mice injected with either  $10^5$  or  $10^6$  CSML-100 cells had extensive metastasis.

The  $\alpha$ -mts-1 antibody detected a high molecular weight band in all samples on the western blot. However, addition of free mts-1 protein to the Western blot when incubating with the  $\alpha$ -mts-1 antibody did not eliminate the signal from the high molecular weight band. Only the

lower molecular weight band found in CSML-100 injected mice was eliminated by competing free mts-1 protein. Therefore, only the lower molecular weight band is mts-1 protein. The higher molecular weight band may be an abundant serum protein which cross-reacts with the  $\alpha$ -mts-1 polyclonal antibody.

FIG. 15c illustrates that the mts-1 protein detected in serum is not a normal component of whole blood and is not a result of a chronic immune response. The mts-1 protein is not detected in lysed whole blood cells (FIG. 15c, Lanes 1-4 containing 5, 10, 20 and 25  $\mu$ l lysed whole blood).

However, mts-1 was detected in similarly treated CSML-100 cells which were provided as a positive control (FIG. 15c, Lane 5).

FIG. 15d illustrates that the mts-1 protein detected in sera of metastatic cancer patients is not due to a chronic immune response induced by salmonella LPS over an extended period of time. The mts-1 protein could not be detected in the 75  $\mu$ g, 100  $\mu$ g or 150  $\mu$ g of sera from chronically immunologically stimulated mice (FIG. 15d, Lanes 1-3).

Accordingly, a 10-12 Kd mts-1 protein can be detected in sera of mice with metastatic cancer. No mts-1 protein is detected in the serum of control mice.

Human Studies: FIG. 16 illustrates that mts-1 protein can be detected only in sera from patients known to have metastatic cancer. An approximate 27 Kd mts-1 protein could be detected in serum from a patient with metastatic breast cancer (FIG. 16, Lane 6) and in two patients with metastatic lymphomas (FIG. 16, Lanes 5 and 7).

However, no such 27 Kd mts-1 protein was detected in serum from a normal patient (FIG. 16, Lane 3) or in serum from patients with non-metastatic breast cancer (FIG. 16, Lane 1) or non-metastatic lymphomas (FIG. 16, Lanes 2 and 4).

The higher molecular weight band apparent in FIGS. 16a-d is not mts-1 protein. In particular, when the Western blot is probed with  $\alpha$ -mts-1 antibody in the presence of free mts-1 protein, only the 27 Kd protein band disappears. Free mts-1 protein does not eliminate the high molecular weight signal. Therefore, the  $\alpha$ -mts-1 polyclonal antibody may cross-react with an abundant serum protein. Such cross-reactivity can be eliminated by, for example, using an antibody directed against human mts-1 protein ( $\alpha$ -mts-1 is directed against mouse mts-1 protein) or by employing highly specific monoclonal antibodies prepared as described in Example 10.

Accordingly, mts-1 protein is detectable only in sera from patients with metastatic cancer. The mts-1 protein cannot be detected in the serum of normal patients or in the serum of patients with non-metastatic cancer. Antibodies directed against mts-1 protein can therefore be used in a simple serum immunoassay to diagnose and detect metastatic cancer in patients.

EXAMPLE 18  
Materials and Methods

Plasmids

5           The coding region of mts1 was cloned in pSK3  
(Pharmacia) vector, containing simian virus promoter.  
The resulting construct was named as pSV-mts1. In pHMG-  
mts1 the coding part of mts1 with the first intron was  
cloned in pHMG vector, containing the constitutive  
10 promoter of hydroxymethyl-glutaryl-CoA-reductase (HMGCR).  
PSVBc12 was constructed by cloning the Bc12/Xho1 insert  
from PEBS7-425 in pSK3 vector.

          The following mouse wild type p53 PCRs were  
designed: #1 - full size coding region (390 aa) was  
15 amplified using primers: forward  
CGGGATCCGACTGGATGACTGCCATGGA (SEQ ID NO:10) (having a BamHI  
site), reverse CGAAGCTTCAGTCTGAGTCAGGCCCCACT (SEQ ID NO:11)  
(including a HindIII site); #2 - N-terminal domain (106  
aa): forward, same as the forward primer for #1, and  
20 reverse CGAAGTCTTGAAGCCATAGTTGCCCTGGTAAG (SEQ ID  
NO:12) (including a HindIII site); #3 - DNA-binding domain  
(185 aa): forward CGGGATCCCACCTGGGCTTCCTGCATGCT (SEQ ID  
NO:13) (including a BamHI site), reverse  
CGAAGCTTGGACTTCCTTTTTTGCGGAAATTTTC (SEQ ID NO:14) (including a  
25 HindIII site); #4 - C-terminal (99 aa): forward  
CGGGATCCCTTTGCCCTGAACTGCCCCCA (SEQ ID NO:15) (including a  
BamHI site), and reverse - same as the reverse primer for  
#1. The PCR products were digested with BamHI/HindIII  
and cloned in eukaryotic expression vector pXmyctag,  
30 containing a CMV promoter and 8-aa myc tag, and bacterial  
expression vector pQE30 (Qiagen). PSP65m65 plasmid DNA  
was used for the amplification of p53. Human pC53-SN3

(human wild type p53) and pC53-SCX3 (human mutant Human mutant p53 -pC53-SCX3 (143<sup>Val-Ala</sup>) eukaryotic expression plasmids were obtained. For conditional expression, mts1 cDNA was excised, cloned in pUHD 10-3 and used for transfection of cell lines producing reverse tetracycline-controlled transactivator (pUHD172-neo) (Clontech).

p21/WAF-luc was constructed by cloning 13 copies of p53 binding consensus element from the p21/WAF promoter in the pFLUC reporter construct containing the Photinus pyralis luciferase gene under the minimal c-fos promoter Saksela et al. (*Mol. Cell. Biol.* 13:3698-3705, 1993). The  $\beta$ -galactosidase expression plasmid was purchased from Clontech. pBabe-Hyg contains Hygromycin-resistance gene. pSV2-neo contains neomycin resistance gene.

#### Cell lines and transfection

Mouse mammary adenocarcinoma cell lines: CSML-0 and CSML-100 Senin et al. (*Exp. Oncology USSR* 5:35-39, 1983), VMR-liv Senin et al. (*Vestnik USSR Acad. Med. Sci.* 5:85-91, 1984) were derived from two independent spontaneous tumors in A/Sn mice. Saos-2 is a human osteosarcoma cell line.

Cells were transfected by electroporation:  $1-3 \times 10^6$  cells in 100  $\mu$ l of phosphate saline buffer were transferred into electroporation cuvette and single pulse of 250V and 250  $\mu$ Fd was applied using Bio-Rad electroporation system. Clones were selected in the presence of 400  $\mu$ g of G-418, for the conventional tetracycline inducible clones, double selection with G-418 and 200  $\mu$ g/ml Hygromycin was used. In transient

transfection experiments, the efficiency of each transfection was monitored by use of a cotransfection of  $\beta$ -galactosidase expression vector, pCMV-gal. At 24-48 hours posttransfection, cells were lysed and the luciferase activity was measured with a luminometer (Promega Corp.). The same lysates were tested for  $\beta$ -galactosidase activity by using o-nitrophenyl- $\beta$ -galactopyranoside (Sigma) as a chromogenic substrate.

#### Preparation of recombinant proteins

Histidine-tagged p53 and Mts1 proteins were expressed in XL-blue Escherichia coli by induction with 0.2 mM isopropyl  $\beta$ -D-thiogalactopyranoside for 4 hours at 37°C. Protein isolation in denaturing conditions followed by renaturation were performed according to the manufacturer's protocol (Qiagen).

#### Western blotting

Protein isolation and western blotting were performed according to Grigorian et al. (*Int. J. Cancer* 67:831-841, 1996) (IJC). Immunostaining and protein bands visualization with ECL system SuperSignal® (Pierce) were carried out according to the manufacturer's protocol.

#### Indirect immunoprecipitations and *in vitro* pull-down assay.

Cells were metabolically labeled for 4h in methionine-cystein-free medium supplemented with dialyzed and inactivated 10% FCS with 0.2mCi/ml [<sup>35</sup>S]-methionine and -cystein (Amersham). The cells were lysed in 150mM NaCl-50mM Tris-Hcl pH 7.6 -0.5% NP-40 and precleaned on

50% protein A-Sepharose. The precleaned lysates were incubated for 2 hours with anti-p53 antibodies: monoclonal pAb421 and goat polyclonal E-19 (Santa Cruz Biotechnology, Inc.) and anti-Mts1 rabbit serum, followed by 5 washes with the same buffer. The precipitated proteins were separated on gradient 4-20% PAAG and detected by autoradiography.

For in vitro pull down assay, 1 µg recombinant Mts1 was mixed with recombinant full size p53 and its domain peptides in 150mM NaCl-50 mM Tris-HCl pH 8.0 - 0.5% NP-40 and precleaned on Protein A-Sepharose on the presence of protease inhibitors at 1 hour in cold room. To the precleaned mixtures, fresh portions of the protein A-sepharose and the corresponding anti-p53 antibodies were added: pAb421 for full-size and C-terminal domain, pAb240 for DNA-binding core domain and E-19 for the N-terminal domain, and incubated for 2 hours in the cold room. Following 5 washes, immunoprecipitates were denaturated by heating at 100°C-5 min, separated in 15% PAAG and transferred to Immobilon-P (Millipore). To detect the co-immunoprecipitated Mts1 protein, membranes were probed with anti-Mts1 antibody and developed by the ECL System. Recombinant human wild type GST-p53 and GST-p53-Δ30 (deletion mutant lacking amino acid residues 364-393) fusion proteins were used for pull down experiments with the Mts1 recombinant protein. 5µg of GST and GST-fusion proteins coupled with Glutathione-sepharose beads were incubated with 2µg of the Mts1 protein in NP-40 buffer (1% NP-40, 50mM Tris-HCl pH 8.0-150 mM NaCl) for 2h in the cold room with rotation. Beads with proteins bound were washed 5 times with NP-40-buffer. Proteins

were isolated by boiling in the protein loading buffer for 5 min and analyzed using Western blotting.

#### Phosphorylation assays

Reactions were performed in a mixture (2 $\mu$ l) containing 50 mM Tris-HCl pH 7.6, 0.2 M NaCl, 10 mM MgCl<sub>2</sub>, 4mM CaCl<sub>2</sub>, 2 mM dithiothreitol, 15 $\mu$ l ATP (Amersham Pharmacia Biotech), 25  $\mu$ Ci [ $\gamma$ -<sup>32</sup>P]-ATP (5000 Ci/nmol, Amersham Pharmacia Biotech), 1 $\mu$ M recombinant wild type p53 or this protein fragments for 30 min at 30°C. PKC assay was done in the presence of 7.5  $\mu$ g of phosphatidylserine (Sigma) by 0.025  $\mu$ g PKC (Roche). CKII was purchased from New England BioLabs Inc., and 50 units were applied per each reaction. Recombinant Mts1 was used in concentrations of 3,5 and 9  $\mu$ M reactions were terminated by 15% SDS-PAGE. Gels were fixed in 10% trichloroacetic acid, dried and exposed to Kodak x-ray film.

#### Electromobility shift assay (EMSA)

Nuclear extracts were prepared as previously described by Kustikova et al. (*Mol. Cell Biol.* 12:7095, 1998). To perform EMSA, nuclear extracts were incubated with end-labeled oligonucleotides that contained binding sites for p53 or Oct-1 proteins. Oligonucleotide sequences were as follows: for Oct-1 - TGCGAATGCAAATCACTAGAA (SEQ ID NO:16) (LeBowitz J.H., *Genes Dev.* 2, 1227-1237, 1998); for p53 - GAACATGTCCCAACATGTTG (SEQ ID NO:17), derived from the promoter of p21/WAF Avantaggiati et al. (*Cell* 89:1175-1184, 1997). The reactions were carried out in 10 $\mu$ l of the buffer containing 100 mM KCl, 1mM MgCl<sub>2</sub>, 1mM DTT,



0.1% NP-40, 0.5mg/ml BSA, 5% glycerol. To perform gel supershift analysis, anti-p53 antibody (pAb421) were added to the EMSA reaction mixtures. The incubation with antibody was carried out for 1 h at 4°C after the binding reactions were completed.

#### Northern blot analysis

CSML-0 conventional Mts1-tet-inducible clones were grown at low and dense conditions and induced with 2µg/ml Doxycyclin at 0.24, 48 and 72h. RNA was isolated according to Chomczynski et al. (*Anal. Biochem.* 162:156-159, 1987). Gel electrophoresis and Northern blot analyses were performed as it is described in Grigorian et al. (*Int. J. Cancer* 67:831-841, 1996). The filters were sequentially hybridized with murine p21/WAF, Bax and Cyclin G1 probes. The amounts of mRNA on the filters were calibrated by hybridization with  $\gamma$ -<sup>32</sup>P-ATP-labeled poly(U) probe. To quantify the intensities of the bands membranes were scanned using a Molecular Dynamics computing densitometer (Sunnyvale, CA) with ImageQuant software, after each hybridization.

## EXAMPLE 19

### MTS-1 BINDS TO THE C-TERMINAL DOMAIN OF P53

5 To determine whether Mts-1 and p53 proteins  
directly interact with each other,  
immunoprecipitation(IP) and Far Western experiments were  
performed. In these experiments, two cell lines were  
used: CSML-0 cells which express very low level of wt-p53  
and does not express Mts1 at all, and CSML100 cells which  
10 express mutant p53 and high level of Mts1.

CSML-0 were transfected with tet-inducible  
Mts1. Lysates from metabolically labeled cells were used  
for IP with anti-p53 and anti-Mts1 antibodies. As shown  
in the IP - radioautography assays following SDS-PAGE  
15 electrophoresis (Figure 17), the p53 protein band was  
readily detected in anti-Mts1 immunoprecipitates and,  
vice versa, the Mts1 protein band in anti-p53  
immunoprecipitates. As a positive control, the band  
corresponding to the heavy chain of the non-muscle  
20 myosin, a known target of Mts1, was also detected in the  
anti-Mts1 immunoprecipitates.

Non-radioactive IP assays with the lysate  
obtained from  $1 \times 10^9$  CSML-100 cells were performed using  
several anti-p53 antibodies targeting different epitopes  
25 located at N-terminal and C-terminal domains of p53.  
Immunoprecipitates were subjected to Western blot  
analysis and probed with anti-Mts1 antibody. The Mts1  
protein was easily detected in the complex precipitated  
by pE19 antibody, directed to the N-terminal domain of  
30 p53. The Mts1 protein was not detected in the complexes  
precipitated by antibodies against C-terminal domain of  
p53, pAb421 and p122Ab (Figure 18).

To identify the domain of p53 that interacts with Mts1, the recombinant p53 domains corresponding to N-terminal (transactivation) AA 1-106, core (DNA-binding) AA 104-288 and C-terminal (oligomerization and regulation) AA 289-387 were obtained. Full-size p53 and above mentioned domains were co-immunoprecipitated with Mts1 recombinant proteins by anti-p53 antibody. Immunoprecipitates were subjected to Western blot analysis using anti-mts1 antibody. As is shown in Figure 19, only full-size p53 and the C-terminal domain of p53 immunoprecipitated the Mts1 protein, but not the N-terminal and the DNA-binding domains.

To more precisely map the interaction site, the recombinant wt-p53-GST and  $\Delta$ 30p53-GST (mutant p53 lacking amino acids 364-393 of the C-terminal domain), captured on the Glutathione-Sepharose4B beads, were incubated with recombinant Mts1. Mts proteins bound to wild type or mutant p53 were recovered in SDS-protein loading buffer by boiling followed by PAGE, Western blotting and immunoprobng with anti-Mts1 antibody. Figure 20 illustrates that p53 molecule with deletion in the C-terminal domain was not able to bind the Mts1 protein, and thus, that the binding site is spread along 364-393 aa of p53.

Another approach, Far-Western blot analysis, was also employed to assess the interaction between Mts1 and p53. Full size p53 and its functional domains, expressed in E.coli, were separated on SDS-PAGE and transferred into Immobilon-P. Filters were incubated with recombinant Mts1 in conditions allowing the interaction with the proteins fixed on the membrane. Mts1 bound to p53 proteins on the filter, was detected

5

with anti-Mts1 antibody. Data shown in Figure 21, consistent with the IP results, indicated that Mts1 was able to bind full-size p53 and its C-terminal domain. As a positive control we have used recombinant fragment of non-muscle myosin which is known as a target for Mts1 protein (Figure 21, lane 5). BSA loaded in 5x excess did not reveal nonspecific mts1 binding in Far-Western assay, neither did N-terminal or DNA-binding domains.

## EXAMPLE 20

### MTS1 PROTEIN INHIBITS PHOSPHORYLATION OF P53 BY PKC

5 The C-terminal domain of p53 contains PKC and  
CKII phosphorylation sites. Experiments were carried out  
to determine whether Mts1 affects the phosphorylation of  
p53. One micromolar recombinant full-size p53 and its  
distinct domains were phosphorylated by PKC in the  
absence and presence of 3, 5 and 9  $\mu$ M recombinant Mts1  
10 protein, respectively, and subsequently analyzed by SDS-  
PAGE.

As shown in Figure 22, Mts-1 inhibited the  
phosphorylation of full-size p53 and the C-terminal  
protein fragment by PKC. Addition of the same  
15 concentrations of Mts1 to the PKC reaction mixture did  
not affect the phosphorylation of the N-terminal and DNA-  
binding domains of p53. No interference of Mts1 was  
shown with CK II phosphorylation of p53 and its domains  
(Figure 23). These observations indicate that Mts1  
20 specifically inhibited the phosphorylation of PKC of the  
C-terminal domain of p53.

## EXAMPLE 21

### INHIBITION OF P53 DNA-BINDING ACTIVITY BY MTS1

Effects of the Mts1-p53 interaction on the DNA-binding activity of p53 were investigated in an electrophoretic mobility shift assay (EMSA) (Figure 24).

The end-labeled oligonucleotide containing p53-binding site from p21/WAF promoter was mixed with nuclear extracts containing wild type p53 (lanes 1). Specificity of the DNA-protein complexes was confirmed by supershift of the complexes after adding anti-p53 antibody (lanes 7), competition with specific p21/WAF p53 binding site-containing oligonucleotide (lanes 2-5) and absence of influence of non-specific nucleotide (lanes 6,14-16). Incubation of nuclear extracts with the Mts1 protein before adding the labeled oligonucleotide decreased DNA-binding activity of p53 in dose-dependent manner (lanes 8-10). The inhibition was less when Mts1 was added after formation of p53-DNA complexes. Mts1 did not affect the binding Oct-1 factor to oligonucleotide containing Oct-1 binding site (lanes 15).

These results indicate that Mts-1 inhibited the DNA-binding activity of p53.

## EXAMPLE 22

### MTS1 AFFECTS P53-DEPENDENT TRANSCRIPTION

5 Mts1 cDNA was placed under the control of HMGCG  
promoter and was cotransfected with constructs bearing  
p53-binding sites from the p21/WAF promoter, fused with  
the luciferase reporter gene. Three different mts1-  
negative cell lines, mouse low (VMR-liv), nonmetastatic  
(CSML-0) adenocarcinoma cell lines with wtp53 and p53-  
10 null Saos-2.1109 cells, were used in this assay. A pCMV-  
 $\beta$ -gal plasmid was cotransfected for evaluation of the  
transfection efficiency and the degree of apoptosis.  
Luciferase activity was adjusted by  $\beta$ -galactosidase  
activity in each transfection. The results of the 2-3  
15 experiments are summarized in Figures 25A and 25B.

The results indicated that Mts1 affected the  
transactivation activity of p53. In all analyzed cell  
lines, the presence of Mts1 correlated with the  
inhibition of the luciferase activity transcribed from  
20 the promoter containing the p21/WAF p53-binding  
consensus. The inhibition was 2-3 folds in CSML-0 and  
VMR-liv, and 1.3-1.4 fold in Saos-2.1109 cells.

### EXAMPLE 23

#### ANTI-MTS1 ANTIBODY ENHANCES TUMOR NECROSIS AND INHIBITS METASTASIS.

5           Mice bearing highly metastatic CSML-100 tumors  
were treated with anti-Mts1 antibody from the initial  
stages of tumor development via i/v injections. In 4  
weeks animals were sacrificed. Tumors, lungs and livers  
were subjected to histological analysis (Figure 26).  
10       Large necrotic areas were observed in tumor mass treated  
with anti-Mts1 antibody (A,right) compared to tumors  
treated with control IgG (A,left).

          Decrease of metastases was observed in lungs  
among animals treated with anti-Mts1 antibody (B,C)  
15       compared to control animals (D,E).

          One experiment with 4 animals in each group was  
done.